

FIG. 1

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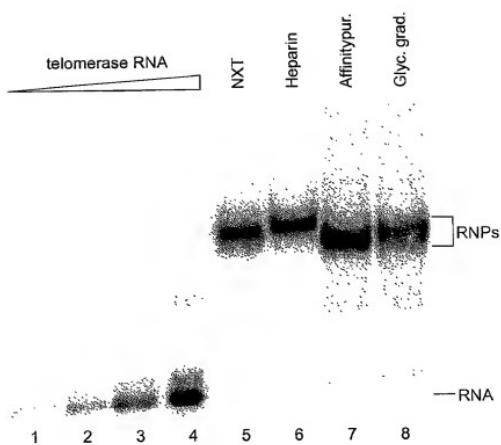


FIG. 2

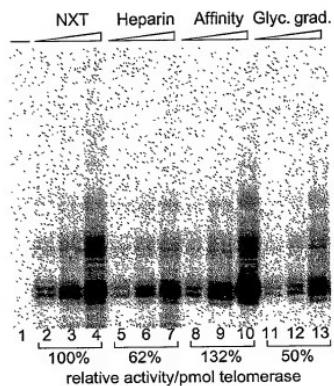


FIG. 3

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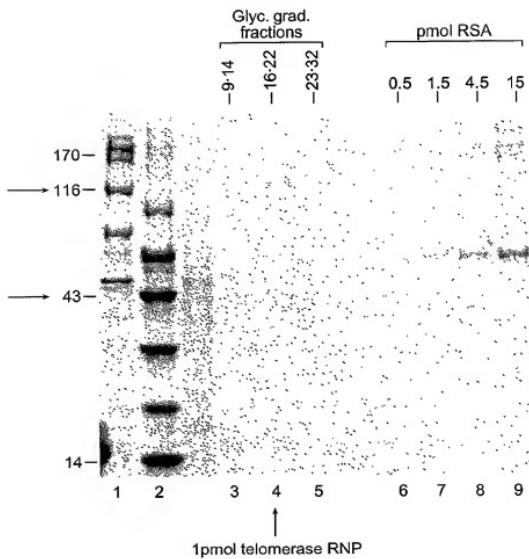


FIG. 4

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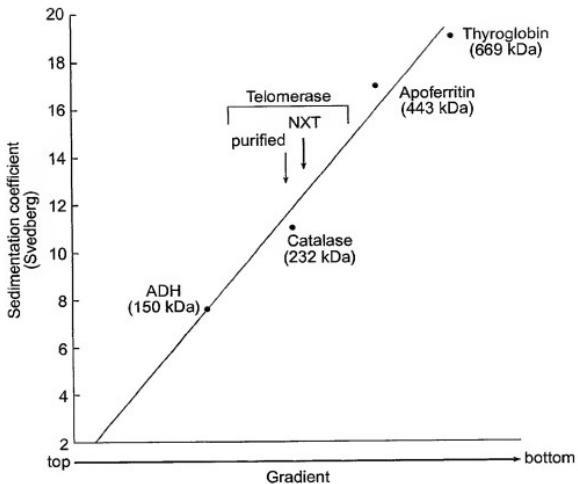


FIG. 5

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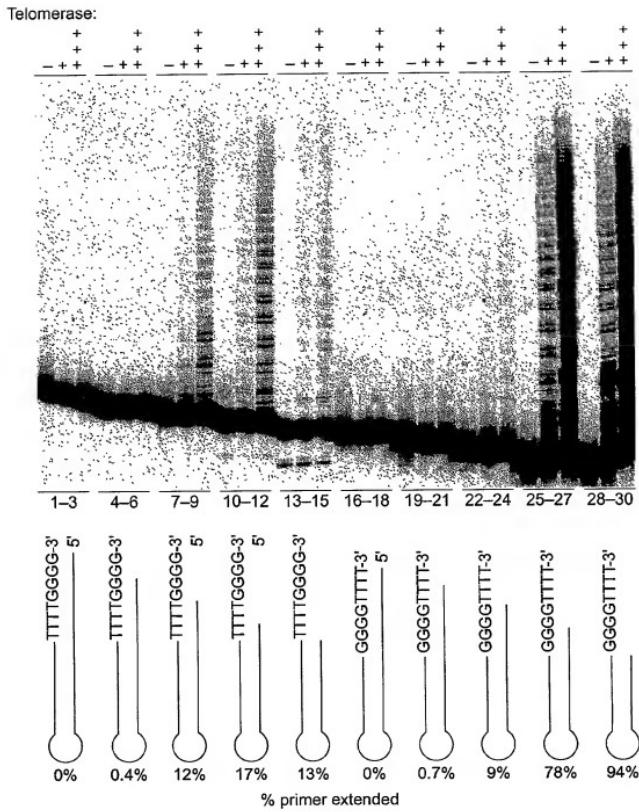


FIG. 6

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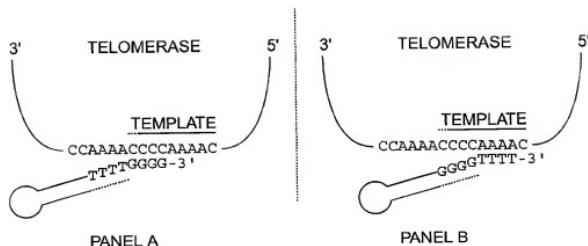


FIG. 7

1 CCCAAACCC CCAAAACCC AAAACCCCTA TAAAAAAAGA AAAATTGAG  
 51 GTAGTTTAGA ATAAAAATAT TATTCGGCGCA CAAATGGAGA TGATATTGA  
 101 TTTGGATGAT ATAGAAAAT TACTCCCTAA TACATTCAC AGATATAGCA  
 151 GCTCTTGATG TGACAAGAAA GGATGCAAAAT CATTGAAATTC TGCTCGAAA  
 201 TCGCTTCAT TGACTTATCC AGAATGCGAA AAACAAATTAA AGTTCTACTT  
 251 CTCGGAATGCA ATATTTTATA ACAGATTCTT CTGGAGAAAA TTAGTTTTAA  
 301 AAAGCAGGAGA CCAAAAGAGTA GAAATGAAA CATTACTAAT GTTAAATAAT  
 351 AATCAGGTTA TGAGGATTAT TCTATTTTTAG AGATCACTTC TTAAAGGAGCA  
 401 TTATGGAGAA AATTACTTAA TAACTAAAAGG TAACAGTTT GGATTTATTC  
 451 CCTAGCCAAC AATGATGAGT ATATTTAAATT CATATGAGAA TGAGTCAAAG  
 501 GATCTCGATA CATCAGACTT CCAAAAGACAA ACTCGCTTAT AAAACCGCA  
 551 AAAAGGTGTTG ATTAATCGAAC AGCAGAGAAA CTTAATGCGAT TTACTATTG  
 601 TATGGTTTTT ATTACATATTG TTTTAGGTAT CGACGGTGA CTCCCGAGTC  
 651 TTGGAGACATAT TGAAAGAACAT GTTACACACT GAAGGAATCA CAGTCTGAA  
 701 AGTTCTGATG TGATGCCAT TATTTTGTA ATTAAATCTCA ATATATCTTAT  
 751 CTCAAATTAA TGAGATGCTG TAGAAAACAA CCAAAATAAAC CATGCAAGTT  
 801 TAATGGAAAT TAAGTGTAAAT CTTTGGGAA AATGCGCACAC TGAAATTATA  
 851 TTGGGATTCAT AAAGCATAGA TACACAGGAT GCTTTAGAGAA CTGATTTAGC  
 901 TTACACACAGA TTACCTGTT TGATTACTCT TGCTCATCTC TTATATCTT  
 951 AAAAGAAGGCA GGCAGAAATG AAGAAAGACAT AAAGAAAGAG ATTTCAAAAT  
 1001 TTGTTGATTC TTCTGTAACCG GGAAATTAACG ACAGAAATAT TAGCAACGAA  
 1051 AAAGAAGAAG AGCTATCACA ATCTCGATTT TAAAGATT TTAAAGATT CAAAATTCC  
 1101 AGGTAAAGAGA GATACATICA TIAAAATCTCA TATATTATAG TTTTTCTATT  
 1151 CACAGCTTTG ATTTCTTTT ATCTTAACAA TATTTTTGAG TTAGCTGGA  
 1201 GTAAAAGATA CTCAAATAGA GAGCGCTAG ACTGAGGTTA CTAGCTTAT  
 1251 TCA-CATTCAT AGATCGACCT TCATATATCC AATACGATGA TAAGGAAACA  
 1301 GCAGTCATCC TTTTTTAAAAA TACTGCTATG AGGACTAAAT TTTCAGAGTC  
 1351 AAGRAATGCA GCGCAATCT TAATCAAAGA GAATTGCGTC GATATTGCA  
 1401 ARGAATCGAA CTCTAAATCT TTGTTTAATA AGTATTACCA ATCTTGATTG  
 1451 ATTGAAAGAGA TTGACGAGGC AACTGACAGC AGATCATTAA AGAAATAAA  
 1501 GTAACTTTTA TTAAATTAGAG AATTAACAAAT ATTACTAATA TAGAGATCAG  
 1551 CGATCTTCAA TTGACGAAAT AAAAGCTGAA CTAAAGTTAG ACAATAAAAA  
 1601 ATACAAACCT TTGTCAAAT ATTGAGGAGA GAAAAGAAGA CCAGTTAGCA  
 1651 AAGGAAAAAAT TAAGGCAATA AATTAATGAG TACAGAAAGT GAAGAAATAA  
 1701 AAGATTATAT TTTCATAATA ATTATTGAGA AGAGGGGTTT TTGGGGTTT  
 1751 GGGGTTTGG GG

FIG. 11

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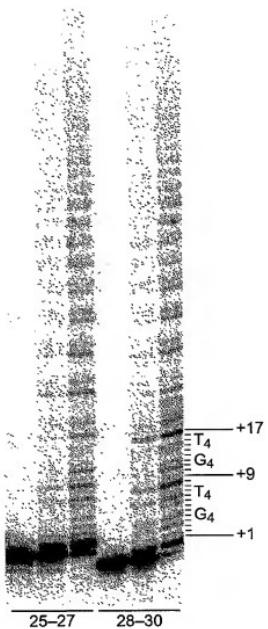


FIG. 8

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1 AAAACCCCA AACCCTTTAG CCCCTTTAG AGCCCTGAG TTGGAAATAT  
 51 AACCTCAGTA TTAATAAGCT CAGATTTTAA ATATTAATTA CAAAACCTAA  
 101 ATGGAGGTG ATGTTGATATA TCAAGCTGAT AATCATGGCA TTCACTCAGC  
 151 TCTTAAGACT TGTTGAGAAA TTAAAGAAGC TAAAACGTTG TACTCTTGGA  
 201 TCCAGAAAGT TATTAGATGA AGAAATCAT CTCAAAGTC TTATAAAGAT  
 251 TTAGAAAGATA TTAAATATG TGCAGACAGA AATAATTGTTG CTACTCCACG  
 301 AGACTATAAT GAAGAAGATT TAAAGTTAT TGCAAGAAAA GAAGTATTTT  
 351 CAACTGGACT AATGATCGA CTTATTGACA AATGCTTAAGT TGAACCTCTT  
 401 TCATCAAGCG ATGTTTCAGA TAGACAAAAA CTTCATGAT TTGGATTICA  
 451 ACTTAAGGG AATCAATTAG CAAAGACCCA TTATTAACA GCTCTTCAA  
 501 CTCAAAAGCA GTATTTCTT CAAGACGAT GGAAACCAAGT TAGAGCAATG  
 551 ATTTGAAATG AGCTCTTCGG ACATCTCTAC ACTAAATATT TAATATTCCA  
 601 CGCAACTGAGA GAAGAACCT TGTTCAAT TTGGCGGGAT AACGTTTTG  
 651 ATCATTTGAA AGTCACAGT AGTTTGCATA AAAAGAAAA AGGTGAGCA  
 701 CGAGACATGA ATGAAACCTCG ATGTTGATCA ACCTGCAAAT ACAATGTCAA  
 751 GAATGAGAAA GATCACTTTC TCAACAAACAT CAACTGCGG ATTGGAATA  
 801 ATATGAAATC AAGAACCCAGA ATATTTTATT GCACTCATTT TAATGAAAT  
 851 AACAATTCCT TCAAAAGAGA TGAGTTGAG AGTAACAAAA ACAATATTTC  
 901 AGCGATGCC AGAGCTCAGA CGATATTCAC GAATATATTC AGATTTAATA  
 951 GAATTAGAA GAAGGACTAA GATAAGGTG TGCAAAAAAT TGCCTACATG  
 1001 CTTGAGAAAG TCAAGATTG TAACTTCAC TACTATTTAA CAAAATCTTG  
 1051 TCCCTCTTCA GAAAATGGC GGGAAACGGAA ACAAAACAT GAAAACCTGA  
 1101 TAATAAACAC TAGAGAAGAA AATGTCAGT ACTATGAGA GCTGTTTAC  
 1151 TACACAACTG ATAATAAAATG CTCACACAA TTATTAATG ATTTCCTCA  
 1201 CARATATACG CCCCCAAAGACT TTTTGACTGG AGAAACACGT AGAAATTTC  
 1251 AAAAGAAAGT TAAGAACATA TGTTGAACTAA ACAAGCATGA ACTCATTAC  
 1301 AAAAACCTTATG TCTGGAGAA GATCAATCA AGAGAAATAT CATGGATGCA  
 1351 GGTGAGACCC TCTGCAAGC ATTITTTATA TTTTGATCAC GAAAACATCT  
 1401 ACGCTTATTA GAAATTGTC CGATGGATAT TCGAGGATCT CGTCCTCTCG  
 1451 CTGATTAGAT GATTTTCTA TGTCCCGAG CAAACAGAAA GTTACTCCAA  
 1501 AACCTTATTAC TCAAGAGCA ATATTGGGA CGTCATTATG AAAATGTCAA  
 1551 TCCGAGACTT AAAAGAGGA ACCCTTGGCT AGGTCCAAGA AAAAGAGGTT  
 1601 GAGAAATGGA AAAAGTCGCT TGGATTGCA CCTGGAAAAAC TCAGACTAT  
 1651 ACCGAAGAAA ACTACTTTG GTTCACATTAT GACTTTCAAT AGGAAGATTG  
 1701 TAAATTTCAGA CCGGAAGACI ACAAAATTAA CTACAAATAC GAAGTATTG  
 1751 AACTCTCACTA TAATGCTTA GACATTGAA AGATAGATOT TTAAAGATCC  
 1801 TTTTGATTG GCTGTTTTA ATCATGATGA TGTAAATGAAA AAGTATGAGG  
 1851 AGTTTGTGTTG CAATGGAAG CAAAGTGGAC ACCAAAACAT TTCTTTGCA  
 1901 ACTATGGATA TCGAAAGATG ATATGATAGT GTAAACAGAG AAAAATCTATC  
 1951 AACATTCTTA AAAACTACTA AATTACTTTC TTCAAGATTTC TGGAATTATG  
 2001 CTGCACAAAT TCTAAAGAGA AAAGATAACA TGTATATCGA TTGGAAAAAC  
 2051 TTTAGAAAGA AAAAGATGAA AGATTATTTT AGACAGAAAT TCCAGAAAGT  
 2101 TGCACTTGA GGAGGACAAAT ATCCAAACCTT ATTCAGTGTG TTGAAATATG  
 2151 AACAAATGAA CTAAATGCA AAAGAAAAT TAAATTGGA AGCAAAAGCAA  
 2201 AGAAAATATT TTAAAGAAGA TAATCTACTT CAACCGATCA TTAAATATTG  
 2251 CCAATATAAT TACATTAAC TTAATGGGA GTTTTATAAA CAAACAAAAG  
 2301 GAATTCTCA AGGTCTTGTG GTTTCATCAA TTTTGTCACTC ATTATTTATT  
 2351 GCAACATTAG AGGAAAGCTC CTTAGGATTC CTTAGAGATG AATCAATGAA

FIG. 9

2401 CCCCCTGAAAAT CCAAAATGTTA ATCTTCTTAAT GAGACTTACA GATGACTATC  
 2451 TTTTGATTAC AACTCAAGAG ATAATGCG TATTGTTTAT TGAGAACCTTC  
 2501 ATAAACGTTA GTCGTGGAAA TGGAATTTAA TTCATAATGAA AGAAACTACA  
 2551 GACTAGTTT CCATTAAGTC CAAGCCAAATT TGCAAAATAC GGAATGGATA  
 2601 GTGTTGAGGA GCAAAATATT GTTCAAGAATT ACTGCGATTG GATTGGCATC  
 2651 TCAATTGATA TGAAAACATT TGTCTTTAATG CCAAAATATTAA ATCTTGAGAAAT  
 2701 AGAAGGAATT CTGTGTACAC TCAATCTAAAC CATGCAAACA AAGAAAGCAT  
 2751 CAATGTGGCT CAAGAAGAAA CTAAAGTCGT TTTAAATGAA TAACATTAC  
 2801 CATTATTTTA GAAAGACGAT TACAACCGAA GACTTTGCCA ATAAAACCT  
 2851 CAACAAGTTA TTATATTCAG GCGGTGACAA ATACATGCAA TGAGCCAAAG  
 2901 AAATACAGGAG CCACTTTAAG AGAAACTTAG CTATGAGCAG TATGATGCAC  
 2951 TTAGAGGTAT CTAAAATATT ATACTCTGTA ACCAGAGCAT TCTTTAAATA  
 3001 CCTTGTGTGC AAATTTAAGG ATCAATTTT TGAGGAGGAG CATTATCCAG  
 3051 ACTTTTCTCT TAGCACACTG AACGACTTTA TTGAATATT CGCACAAAAA  
 3101 AAGTACATTTC TCAACAGATG TTGCGATGTC CTCAAGGCAA AAGAAGC  
 3151 GCTAAAAAGT GACCAATGTC AATCTCTAA TCAATATGAT GCATAGTCGA  
 3201 CTATTCTAAC TTATTTGGG AAGTTAATT TCAATTTCGG TCTTATATAC  
 3251 TGGGGTTTGG GGGTTTTGGG GTTTGGGG

**FIG. 9**  
(CONTINUED)

1 MEVDVDNQAD NHGIHSALKT CEEIKEAKTL YSWIQLVKIRC RNQSOSHVKD  
 51 LEDIKIFQAQT NIVATPRDYN EEDFKVIARK EVFSTGLMIE LIDKCLVELL  
 101 SSSDVSDRQE LQCFQFLKG NQLAKTHLLT ALSTQKQYFF QDEWNQVRAM  
 151 IGNELFRHLY TKYLIFQRTS EGTLVQFCGN NVFDHLKVND KPDKKQKGGA  
 201 ADNNEPRCCS TCKYVNKNKE DHFLNNINVE NWNNNMSRTR IFYCHTFNRN  
 251 NQFQKKHGFV SNKNNNSAMD RAQTIPTNF RPNRIRKKLK DKVIEKIAYM  
 301 LEVKVDPNFM YYLTKSCPLP ENWRERKQKI ENLINKTREB KSKYYEELES  
 351 YTTDNKCVTQ FINEFFYVNL PKDFLTGRNR KNFQKKVKVY VELNKHELIH  
 401 KNLLEKINT REISWMQVTEL SAKHFYYFDH ENIYVLUWKL RWIFEDLVVS  
 451 LIRCFFYVTE QQRYSYSKITY YRKNIWDVIM KMSIADLKKE TLAEVQEKEV  
 501 BEWKKSLSGF PGKLRLIPKK TTFRPIMTFN KKIVNSDRKT TLTTINTKLL  
 551 NSHMLKTLR NRMFKDPFGF AVFNYDVMK KYEEFVCKWK QVGQPKLFFA  
 601 TMDIEKCYDS VNRKLSTFL KTTKLLSSDF WIMTAQILKR KNINVIDDSKN  
 651 FRKEMKDVF RQKFQKIALE GGQYPTLFSV LENEQNDLNA KRTLIVEAQ  
 701 RNYFKKDNLN QPVINICQYN YINFNGKFKY QTKGIPQGLC VSSILSSFY  
 751 ATLEESSLGK LRDESMPEN PVNVNLLMRLT DDYLJITTOE NNAVLPIEKL  
 801 INVSRENGFK FNMKKLQTSF PLSPSKFAKY GMDSVBBQNI VQDYCDWIGI  
 851 SIDMKTALAM PNINLRIEGI LCTLNLNMQT KKASMWLKKK LKSFLMNNIT  
 901 HYFRKTITTE DFANKTLNLK FISGGYKYMQ CAKEYKDHFK KNLAMSMID  
 951 LEVSKIYIVS TRAFFKYLVC NIKDTIFGEE HYPDFFLSTL KHFIEIFSTK  
 1001 KYIFNRCMII LKAKEAKLKS DQCQSLIQYD A

FIG. 10

CCCCCAAAACCCAAAACCCAAAACCCCTATAAAAAGRAAAAATTGAGGTAGTTAGA  
 1 +-----+-----+-----+-----+-----+-----+-----+-----+  
 GGGGTTTGGGTTTGGGTTTGGGATATTTCCTTTAACTCCATCAAATCT 60  
 a P Q N P K T P K P L \* K K K K L R \* F R -  
 b P K T P K P Q N P Y K K R K N \* G S L E -  
 c P K P Q N P K T P I K K E K I E V V \* K -  
 AAAAAATATTATTCGGCACAATGGAGATGGATATTGGATGATAGAAAATT  
 61 +-----+-----+-----+-----+-----+-----+-----+  
 TTATTTATAAAGGGCTTACCTCTACCTAAACCTACTATATCTTTAA 120  
 a N K I L P P H K W R W I L I W M I \* K I -  
 b I K Y Y S R T N G D G Y \* F G \* Y R K F -  
 c \* N I P A Q M E M D I D L D D I E N L -  
 TACTTCCTAATACCAACAGTATAGCAGCTCTGTAGTGACAAGAAGGATGCAAA  
 121 +-----+-----+-----+-----+-----+-----+-----+  
 ATGAAGGATATGTAAGTTCATATCGTAGAGACATCACTGTTCTCTAGTTT 180  
 a Y F L I H S T S I A A L V V T R K D A K -  
 b T S \* Y I Q Q V \* Q L L \* \* Q E R M Q N -  
 c L P N T F N K Y S S S C S D K K G C K T -  
 CATTGAAATCTGGCTCGAAATCGCCTCATTGACTATTCAAAGTTGCAAAAACATTAG  
 181 +-----+-----+-----+-----+-----+-----+-----+  
 GTAACTTAGCGAGCTTAGCGGAAGTAAGTAACTGATAAGGTTCAACGTTTTGTTAATC 240  
 a H \* N L A R N R L H \* L F Q S C K N N \* -  
 b I E I W L E I A F I D E Y S K V A K T I R -  
 c L K S G K S P S L T I P K L Q K Q L E -  
 AGTCTRACTTCGGATGCAAATCTTATAACGATTCTTCTTGAGAAAAATTAGTTAA  
 241 +-----+-----+-----+-----+-----+-----+-----+  
 TCAAGATGAAGAGGCCAGCTAGTTAGAAATATTGCTAAGAAGAACTCTTTAATCAAATT 300  
 a S S T S R M Q I F I T I L S \* E N \* F \* -  
 b V L L L G C K S L \* R F F L E K I S F K -  
 c F Y F S D A N L Y N D S F L R K L V L K -  
 AAAGCGGAGAGCAAAGACTAGAAATTGAAACATTACTATGTTAAATAAAATCAGGAA  
 301 +-----+-----+-----+-----+-----+-----+-----+  
 TTTGCCTCTCGTTCTCATCTTAACTTGTAAATGATTACAAATTATTAGTCATT 360  
 a K A E S K E \* K L K H Y \* C L N K I R \* -  
 b K R R A K S R N \* N I T N V \* I K S G N -  
 c S G E Q R V E I E T L L M F K \* N Q V M -  
 TGAGGATTATTCTATTTTTAGATCACTCTTAAGGAGCATTATGGAGAAAATTACTTA  
 361 +-----+-----+-----+-----+-----+-----+-----+  
 ACTCTAATAGATAAAAATCTAGTGAAAGAATTCTGTAATACCTCTTTAAATGAATT 420  
 a \* G L F Y F L D H F L R S I M E K I T \* -  
 b E D Y S I F \* I T S \* G A L W R K L L N -  
 c R I I L F F R S L L K E H Y G E N Y L I -

FIG. 12

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**FIG. 12**  
(CONTINUED)

TTACACAGATTACCTGTTTACTCTTCATCTCITATACTTAAAGAAGAGCA  
 901 AATGTTGCTTAAGGACAAAACAATAGAGAACGGAGTAGAGAAATATAGAANNTTCTCGT  
 a L Q Q I T C F D Y S C S S L I S L K E A -  
 b Y N R L P V L I T L A H A L L Y L \* K K Q -  
 c T T D Y L F F \* L L L D I S Y I F F K R S R -  
 GGCAGAATGAAAAGAGACTAAAGAAGAGATTCTAAATTTGTTGATTCTCTGTGAA  
 961 CGCGCTTACTTCTCTGATTCTTCTCTAAAGTTTAAACAACTAAGAACAGATTTG  
 a G E M K R R L K K E I S K F V D S S V T -  
 b A K \* K E D \* R K R F Q N L L I L \* P -  
 c R N E K K T K E R D F K I C \* F F C R N -  
 GGAATTAAACAAAGAATATTAGCACGAAAGAGAGAGAGCTATCACAACTCTGATT  
 1021 CCTTAATGTTGTTCTTATACTGTTGCTTTCTCTCTGATAGTGTGAGGACTAAG  
 a G I N N K N I S N E K E E E L S Q S \* F -  
 b E L T T R I L S A N E K K K S Y H N P D S -  
 c N \* Q Q E Y \* Q R K R R R A I T I L I L -  
 TTAAAGATTCAAAATCCAGGTAAAGAGAGATACATTCTAAATTCATATATTATAG  
 1081 AATTCTAAAGTTTAAAGGTCATCTCTCTGATGAACTTAAAGTATATAATAC  
 a L K S I S K I P G K R D T F I K I H I L \* -  
 b \* R F Q K F Q V R E I H S L K F I Y Y S -  
 c K D F K N S R \* E R Y I H \* N S Y I I V -  
 TTTTCATTTCACAGCTGTTATTTCTTATCTTAAACATATTTTGATTGCTGGAA  
 1141 AAAAAAGTAAAGTGTGCGACAATAAAAGAAAATAGAATTGTTATAAAAACATCGACCTT  
 a F F I S Q O L L F S F I L T I F F D \* L E -  
 b F S F H S C C Y F L L S \* Q Y F L I S W K -  
 c F H F T A V I F F Y L N N I F \* L A G S -  
 GTAAAAAGTATCAAATAAGAGAGGGCTAGACTGAGGTAACTTAGCTTATTCTACATTCA  
 1201 CATTTTCATAGTTTATCTCTCGCGATCTGACTCCATTGAATCGAATAAGTGTAAAGT  
 a V K S I K \* E K R \* T E V T \* L I H I H -  
 b \* K V S N N K R S A L R \* L S L F T F I -  
 c K K Y Q I R E A L D \* G N L A Y S H S \* -  
 AGATCGACCTTCATATATCCAACTACGATGATAAGGAAACAGCAGTCATCGTTTAAAGA  
 1261 TCTAGCTGAGTATAGGTTATGCTACTATTCCTTGTGCTGAGTAGGCAAAATTTT  
 a R S T F I Y P I R \* \* G N S S H P F \* K -  
 b D R P S Y I Q Y D D K E T A V I R F K N -  
 c I D L H I S N T M I R K Q Q S V L K I -  
 TAGTGTCTATGAGGACTAAATTTTAGGTCAGTCAAGAAATGGAGCGGAAATCTTAACTAA  
 1321 ATACGATACCTCTGATTTAAACATCTCAGTTCTTACCTCGCTGAGTAGAATTTT  
 a \* C Y E D \* I F R V K K W S R N L N Q K -  
 b S A M R T K F L E S R N G A E I L I K K -  
 c V J \* G L N F \* S O R M E P K S \* S K R -

**FIG. 12**  
(CONTINUED)

GAATTGCGTCGATATTGCAAAGAACGAACTCTAAATCTTCGITAATAAGTATTACCA  
 1381 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 1440  
 CTTAACGGCAGCTATAAGCTTTCTTCGCTTGAGATTAGAAAGCAATTATTCATAATGGT  
 a E L R R Y C K R I E L \* I F R \* \* V L P -  
 b N C V D I A K E S N S K S F V N K Y Y Q -  
 c I A S I L Q F N R T L N L S L I S T N -  
 ATCTTGATTGATTGAAGAGATTGACGAGGCAACTGCACAGAAGATCATTAAGAAATAAA  
 1441 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 1500  
 TAGAACTAACTAACTCTCTACTGCTCGITGAGCTGTCTCTAGTAATTCTCTTATT  
 a I L I D C R D \* R G N C T E D H \* R N K -  
 b S \* L I E E I D E A T A Q K I I K E I K -  
 c L D \* L K R L T R Q L H R R S L K K \* S -  
 GTAACTTTATTAACTTAGAGAATAAACTAAATTACTAATATAGAGATCAGCGATCTCAA  
 1501 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 1560  
 CATTGAAAATAATTAACTCTTATTGATTAACTGTTAGTCTAGTCGCTAGAAGTT  
 a V T F I N \* R I N \* I T N I E I S D L Q -  
 b \* L L I R E \* T K L L I \* R S A I F N -  
 c N F Y \* L E N K L N Y \* Y R D Q R S S I -  
 TTGACGAAATAAAAGCTGACTAAAGTTAGACAATAAAACATAACCTTGGTCAAAT  
 1561 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 1620  
 AACCTGCTTTATTCGACTGATTCTCAATTCTGTATTCTTATGTTGGAACAGTTTA  
 a L T K \* K L N \* S \* T I K N T N L G Q N -  
 b \* R N K S \* T K V R Q \* K I Q T L V K I -  
 c D E I K A E L K L D N K K Y K P W S K Y -  
 ATTGAGGAAGGAAAAGAACGAGCTTAGCAAAAGAAAAATAAGGAATAAAATAATGAA  
 1621 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 1680  
 TAATCTCTTCTTCTCTGGTCAATCTGGTTCTTCTTATTCGTTATTCTTACT  
 a I E E G K E D Q L A K E K I R Q \* I K \* -  
 b L R K E K K T S \* Q K K K \* G N K \* N E -  
 c \* G R K R P V S K R K N K A I N K M S -  
 GTACAGAAAGTGAAGAAATAAAAGATTATTTTCTAAATAATTATGAAAAGGGGTT  
 1681 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 1740  
 CATGTCTTCACTCTTCTTCTAAATAAAAAGTTAAATAACTTTCTCCCCAA  
 a V Q K \* R N K R F I F F F N N L L K R G V -  
 b Y R S E E I K D F F S I N I Y \* K E G F -  
 c T E V K K \* K I Y F F Q \* F I E K R G F -  
 TTGGGGTTTGGGGTTTGGG  
 1741 -----+-----+-----+-----+-----+-----+-----+-----+ 1762  
 AACCCCAAAACCCCAAAACCC  
 a L G F W G F G -  
 b W G F G V L G -  
 c G V L G F W -

*FIG. 12*  
(CONTINUED)

2 EVDVQNOADNHGIIHSALKTCEEIKEAKTLYSWIJKVIRCRNQSQSHYKDL 51  
 19 ELELEMQENQNQDIQVRVK...IDDPKQY..LNVNTAACLLQEGSYYYQDK 62  
 52 EDIKIFQAQTNIVATPRDYNEEDFKVIARKEVP..STGLMIELIDKCLVELL 100  
 63 DERRYIITKALL...EVAESDPEFICQLAVVYIRNELYIRTTNYIVAF. 107  
 101 SSSDVSDRQKLQCFGFQLKGQNLAKATHLTLASTQKQYFFQDEWNQVRAM 150  
 108 .....CVVHKTQDFIEKYFNKAFLLPNDLLEVCEFAQVLYI 144  
 151 IGNELPFLHLYTKYLIFQRTSEGTLVQPCGNVFDHLKVNDKFDKKOKGG 200  
 145 FDATERFKNLY.....LDRILSQDIRKELETFRKCLQRQCRVSKF 181  
 201 ADMNE...PRCCSTCKYINVKNEKDHFHNNINVPNWNMKSRTIFYCHF 247  
 182 SEFNEYOLQGRYCTES..QRKKTMFRLSVTNKQXWDQTKKK..... 220  
 248 NRNNQQFFKKHEFVSNKNNSIAMDRAQTIPTNIFRPNPIRKKLKDVKIEKI 297  
 221 .RKENLILTQAIKESEDDKSRKETG...DIMMVEDAIAKLPAPVMKCI 264  
 298 AYMLEKVKDGPNFNYLTKSCPLPENWRERKQKJENLINKTREEXSKYEE 347  
 265 AKRNQNAMEK.....KHMKAPKIPNSTLESKYLTIFKD 294  
 348 LFSYTDTDNKCVTQFINFOFFYNIILPKDFLTGRNRKFQKKVKKYVELNKHE 397  
 295 LIKFCHTISEP....KERVYKILGKVKYPKTEEBYKAAFGDSASAPFN.PE 338  
 398 LIHKNLLLEKINTREISWMQVETSAKHFYYFDHENIYVLWKLRLWIFEDL 447  
 339 LAGKRMKIEKSKTWENELSAKGNTAEVWDMNLISSNQLPYMAMLRNLSN.. 386  
 448 VVSLLRCCFFYVTBQQKSYSKTYYYRKNIWDMKMSIADLKKTETLAEVQE 497  
 387 .....ILKAGVSD..... 394  
 498 KEVEEWKKSLGFAPGKLRLLIPKKTTFRPIMTFNKKLVNSDRKTTKLTTNT 547  
 395 .....TTHS 398  
 548 KLLNSHMLKTLKKNRMFKDLPFGFAVFNYDDVMKKYEEFVCKWKQVGQPKL 597  
 399 IVINK.....ICEPKAVENSKM 415  
 598 FFATMDIEKCYDSVNREKLSTPLKTTKLSSDFWIMTAQILKRKNNIVID 647  
 416 F..PLQFFSAIEAVN.EAVTKGPKAKK...RENNMLKGQIEAVKE..VVE 457  
 648 SKNPKRKEMKDYFRQKFQKIALLEGQGYPTLPSVLENBQNDLNAKKTLIVE 697  
 458 KTDEEKKDM.....ELEQTEEGEFVKVNEGIGKQYINSTELAIK 496  
 698 AKQRNYFKKDNLQPVINICQNYINFNGKFYKOTKGIPQGLCVSSILSS 747  
 497 IAVNKNLDEIKGHTAIFSDVSGSMSTSMSGGAKKYGSVRTCLECALVGL 546  
 748 FYYATLESSLGFLRDESMNPENPNVNLLMRLTDDYLLITTQENNAPLF 797  
 547 MVKQRCEKSSFYIFSSSPSSOCNKCYLEVL..... 576

FIG. 13

798 EKLINVSRENGFKPNMKK..LQTSPPLSPSKFAKYGMDSVEEQNIVQDYCD 846  
 577 .....PGDELRPSMQKLQEKGKLGGS..TDPFYECIDEWTKNKTHVD 617  
 847 WIGISIDMKTALALMPNINLRIEGILCTLNLMOTKKASMWLKKLKSPLM 896  
 618 NIVILSDOMIAEGYSDINVRGSSIVNSI.....KKYKDEVN 653  
 897 NNITHYPRKTITTEDPANKTLNLKFISGGYKYMCAKEYKD.HFKKNLAM 945  
 654 PNIKIF..AVDLEGYG.....KCLNLGDEFNENNYIKIFGM 687  
 946 SSMIDLEVSKIIYSVTRAFFKYLVCNIKUTIFGBEHYPDFFLSTLKHPIE 995  
 688 SDSI.....LKFISAKQGGA.....NNVE 706  
 996 IFSTTKYIIFNRVC 1008  
 707 VI..KNPALQKIG 717

**FIG. 13**  
(CONTINUED)

132 LSTQKQYFFQDEWNQVRAMIGNEL.FRHLYTKYLIFQRTSE..GTLVQFC 178  
 1 MSRRNQ.....KKPQAPIGNETNLDLDFVLQNLLEVYKSQIEHYKTQQQI 43  
 179 GNNVFDHVKVNDKFDKKQKGGAADMNEPRCCSTCKYNVNEKDHDPLNNIN 228  
 44 KEEDLKLKLPKNQDDGNGSNDDDBE.....NNSNKQZELLRRVN 84  
 229 VPKWNNMSRTRIFYCTHONRNQPFKKHEFVSNKNNISAMDRAQTIFTN 278  
 85 .....QIKQVQVQLIKK..VGSKVEKDNLNLNEDENKN 114  
 279 IFRPNRIRKKLKDVKIHKAYMLEKVDPNFTYLTKSCPLPENWRERKQ 328  
 115 GLSEQQVKEEQLRTITEQVVKYQNLVFNMDYQLDLNESQGHRRHRETDY 164  
 329 KIRNLINKTREEKSKYYEELFSYTTDNKCVTQFINE.FFYNILPKDFLTG 377  
 165 DTEKWPEISHDQK.....NYVSITYANQKTSYCWNLKDYFNK 200  
 378 RNRKNPQKKVVKYVETLNKHIELHKNLLLEKINTNREISNMQVETSAKHFYY 427  
 201 NNYYDHLNVSIRNLE..TEAEFYAFPDFSQTIKLTNNSYQTVNID..... 242  
 428 FDHENIYVLWKLRLRWI..FEDLVVSLIRCFYYVTEQQKSYSKTYYRKNI 475  
 243 VNPDNNLCL1ALLNLFLLSLERPNILNIRSSY..TRQYQNFKEKIGELLETI 290  
 476 WDVIIMKMSIAIDLKKTLEAEOKEVEEEWKSLGPAGPKLRLIPKTTFRP 525  
 291 FAVVFSHR.....HLQGIGHLQVPCBAPQYLVNSSSQISVKSQSQLQ 330  
 526 IMTFNKKIVNSDRKTTKLTTNTKLLNSHMLMLKTLKNRMPKDPPGFVAFNY 575  
 331 VYSFSTDKLVD..TNKQDYFKFLQEFPRLTHVSQQAI PVSATNAVNL 378

FIG. 14

576	DDVMKMKYEEFVCKWKQVGQPKLF.	. . . . .	FATMDIEKCYDS..VNREK	615
379	NVLKKVKH	A NLNLVSPTQFNDFPYFVNQLHLKLEPGLBNPLTQK	. . . . .	426
516	LSTFL.	. . . . .	KTTKLLSSDFWIMTAQILKRKNNI..VIDSKNFRKEMK	657
427	LENL LLSI	QKSNLKPLRLNFTYTYAQETSRKQILKQATTINKLNKLNNQ	. . . . .	476
558	DYFRQKFQKIALEGQGQYPTLFSVLEN..EQNDLNNAKKTLLIVEAKQRNYFK	. . . . .	. . . . .	705
477	BETPETKDTEPSESTSGM KFFDHLSLTLEDEDFSVN..LQATEQIY..	. . . . .	. . . . .	520
706	KDNLLQPVINICQNYNINFNGFKYQTKGI	PQGLCVSSILFSSYYATLEE	. . . . .	755
521	.DSLHKLLIRSTNLKKFKLSSYKYE	MESKIMDTFDIDLKNI. . . . .	YETLNN	564
756	SSLGFLRDES	MNPVNPNVNLMLRTDDYLLITTQENNAVLFIEKLINVR	. . . . .	305
565	....LKRCVSNISNP	HGNISYEITN. . . . .	KDSTFYKFKLTLNQE	500
806	ENGPKFNMMKLQLTQSFPPLSPSKPAKYGMDSVEE	QNIVODYCWDIGISIDMK	. . . . .	855
601	LQHAKYTTFK..QNEPQFNNVKS	AKIESSSLSELDIDSICKSIA	CKNLQ	648
856	TLALMPNINLRLEGILCTLNLNMQT..KKASMNLLK..	KLKSLFMNNITH	. . . . .	901
649	NVNI. . . . .	IASLILYPPNNIQKNFNFNKPNLFFFQKOFQPKLNLENVSINC	. . . . .	691
902	YFRKTI. . . . .	TTEDFANKTLNKLFISSGGYKYMCAKEYKDHEKKNLAMSSM	. . . . .	948
692	ILDQHILINSI	SEIFLENKKNKIKAFILKRYLLQQYLDYT	TKLFKTLQQLPEL	741
949	IDLEVKSIYSVT. . . . .	RAFFKYLWCNICKDT..IFGEEHY	. . . . .	982
742	NQVYINQOQLEELT	VSEVHKVWENHKQKAFYEP	LCFIEKCESQTTQLIDF	791
983	PDFFLS	TLKHFIIEIFSTK	YIPNRVCMLKAKEAKLKSQDCQCSLIQ	1028
792	DQNTVSSDSD	I KKLK ILES I SE SKY HYLRLNLPQS	S QSS LIKSEN EEEI QELLK	840

*FIG. 14*  
(CONTINUED)

FIG. 15

1 MEMDIDLDDIENL.....LPNTFNKYSSSCSDKKGCKTLKSGSKSPS...	42
491 IELAIAKIAVNKLDEIKGHTAIIFSDVSGSMSTSMSGAKKYGSVRTCLEC	540
43 .LTIPKLOKO.....LEFYFSDANLYNDSFLRKLVLSGEQRVEIETLL	85
541 ALVLGLMVKQRCEKSSFYIFSSPSSQCNKCYL.EVDLPGDELRPSMQKLL	589

FIG. 16

telomerase p43	LQKQLE <del>PF</del> ESDANLYNDFIRKLVLKSGEQR <del>E</del> IETLLM
human La	ICHQ <del>UEY</del> FFGDFNLPRDKF <del>FIKE</del> QOI. KLDEGWVPLEIMIK
Xenopus LaA	ICEI <del>EY</del> FFGDHNLPRDKF <del>FIK</del> QOI. LLDDGWVPLETMIK
Drosophila La	ILR <del>VEY</del> FFGDANLNRF <del>PIRE</del> QIGKNEDGW <del>PL</del> SLVLT
S. c. Lhp1p	CLK <del>QEV</del> FFSEFNFPYDR <del>FIR</del> TAAEK.NDGW <del>W</del> PISTIAT

FIG. 18

1 aactcattta attacaattt taatcaacaa gattgataaa aagcgtaaa taaaacccaa  
 61 tagatataat tttagaaatgg attagaaatgg aatggaaattt gaaaadcaact aagcacata  
 121 gaaaaaaaggc gaaaatattgtt ggtggaaact tgaatagtag atgcaaaaaaa acaaaaatgaa  
 181 tatataatggt aagggttaaga ttgacatggc taagcaatat ctcgtggaaacg tcactgcac  
 241 atggttttgtt taggaaggta gtttactacta agataaaatg gaaaaggat atatcatcac  
 301 taagaoactt ctggaggcttgc ttggacttgc ttccggatgc atctgcgttgc tgccgtatca  
 361 catccgtatgaa gacttataa tcggaaactact cactaaactatc attgtagcat ttgtgttgt  
 421 ccacaaaggact actcaacatc ttccatggaa gttactcaac aaagcgatggat ttttgcctaa  
 481 tgacttactgtt ggatgttgc aatttgcataa gtttcttcat atttttgtat caactgtt  
 541 caaaaaatttg ttccatggta ggttactctt attagatattt cgtaaaggac tcactttccg  
 601 taatgtttttt ccaaaggatgg cttcaacaa gttttcttgc ttcaacaaatc acactttgg  
 661 taatgtttttt actgttatccc aatgtttttt aatcaatgtt ctttacccatc ctttttttttcc  
 721 caatggaaatgg gttttttttt cttatggaaatgg gggaaaatgg aatcttttttcc  
 781 gggaaatggat ggttttttttgc ttatggatcca gagaaaaatgg gggatccatc tggatccat  
 841 agatgcataatc aaggctttaa aaccggcgttgc ttttttttttgc ttttttttttgc  
 901 catggatccatc cacatggaaatcc ctttttttttgc ttttttttttgc  
 961 gagcttcggatccatc aatggatccatc aatggatccatc aatggatccatc  
 1021 gatcccttgc ttatggatccatc aatggatccatc aatggatccatc  
 1081 tgatccatcgc ctttttttttgc ttttttttttgc  
 1141 aacatggatccatc aatggatccatc aatggatccatc aatggatccatc  
 1201 ttcaatccatc aatccatccatc aatccatccatc aatccatccatc  
 1261 cgggtttttccatc aatccatccatc aatccatccatc aatccatccatc  
 1321 tgatccatcgc aatggatccatc aatggatccatc aatggatccatc  
 1381 agttactaaatggatccatc aatggatccatc aatggatccatc aatggatccatc  
 1441 agaaatggatccatc aatggatccatc aatggatccatc aatggatccatc  
 1501 aaccggatccatc aatggatccatc aatggatccatc aatggatccatc  
 1561 cattggatccatc aatggatccatc aatggatccatc aatggatccatc  
 1621 tggatccatc aatggatccatc aatggatccatc aatggatccatc  
 1681 gtatggatccatc aatggatccatc aatggatccatc aatggatccatc  
 1741 acgttgttgc aatggatccatc aatggatccatc aatggatccatc  
 1801 ttacttgc aatggatccatc aatggatccatc aatggatccatc  
 1861 agagaaatggatccatc aatggatccatc aatggatccatc aatggatccatc  
 1921 aaaaatggatccatc aatggatccatc aatggatccatc aatggatccatc  
 1981 atattccatc aatggatccatc aatggatccatc aatggatccatc  
 2041 tggatccatc aatggatccatc aatggatccatc aatggatccatc  
 2101 taatccatc aatggatccatc aatggatccatc aatggatccatc  
 2161 aatccatc aatggatccatc aatggatccatc aatggatccatc  
 2221 ctttgccttgc aaaaaatggatccatc aatggatccatc aatggatccatc  
 2281 ctcaaaaaatggatccatc aatggatccatc aatggatccatc aatggatccatc  
 2341 atttaatggatccatc aatggatccatc aatggatccatc aatggatccatc  
 2401 aaaaatggatccatc aatggatccatc aatggatccatc aatggatccatc

FIG. 19

	Motif A	Motif B	Motif C	Motif D	Motif E
Consensus	h--hDh--h-h	h--+Q--SP			
telomerase p123	GQPPLFFATMDIERCYDSUNREKULSTFLKTKL-100-KPYQOTKGIPQQLCVSISLSSPFYATLEESSLGFL				
Dong (L1NS)	KNRNLHCTYDIIKCAFOSTPHENWLOTEIYKIN-28-KQIAIKKGIGYQODSLSLNFCCLANPUSGHOLANDR				
al. S. C. (group 1)	FGSNNWPREVDIJKCFITISHLTLIKEKRYTSD-26-HVPGPRVCVQAPISPALCNANLRLDRAGLA				
HIV-RT	LKKKSTVILDGAYASVPLDEDRKYTAIFP-7-GIRYQVNVLPKQNGKSPAFQSMTKILEPFRQN				
1.8543..12	VLPELYMMKPDVKSCYDSLPRAMECRLKALKN-68-KCYIREDGLPQSSILSAPTVIDLVDLLEPYSEFK				
Consensus	h--YIDDhbb	h-h-h--K			
telomerase p123	-14-LFLFLDILLIPTQQNN-0-AVIFIEKJLNGSNGKFKAHKKLT-23-QNYCDWGSQI				
Dong (L1NS)	-16-HLYMD-DKRYANDKE-0-NKLLDITTFSDINQGQDCKCT-25-KGLTKYIGQO				
al. S. C. (group 1)	-55-YVRYADDLILGVGUSNN-2-KLKRDLNNTLNS-LGDTINEEKT-1-ETPARFUGYNI				
HIV-RT	-4-IVYOMD-DIYVSHLEIG-1-IRTKIELRQHLLRWGLTTDEKHO-0-EPPFTWNGYEL				
1.8543..12	-8-IILKLAADPLIISTDQQQ.....VINKELKANGFQYNAKRN-41-IRSKSKSGIPR				

FIG. 17

MEIENNNAQQPKAEKLWWELELEMQENQNDIQVRKIDDPKQYL  
VNNTAACCQLLSSGQSYYQDKDERRYITKALLEVAESDFPFCQIA  
VYIRNELRTTNYIIVACFWVHNKTQPIFEKYFKNVALKFLPNLD  
LECEVFACQVLYFIIDATEFKNFLYLRLLSDQIRKELTFRCLQC  
VRKSFSEFNEYQLGYKCTESQRKTTMFKRFLYSLVNTQKNDQDTKK  
RKENLLTTLQKA1KSEDESK3KRTEDJIMVNEDEA1KALPCKAVMKK  
AKRNQANMKHMKKA1KIPN1STLESVKYTFKD1KCH1SPEVMMK  
YKLIGKQYKPTEEBVEKAAPGDSASAPFPNPELAGKRMKIE1SKTW  
ELASSENKGNTAWEVDNL1NSNQLPYMLARNLNSLN1KAGVSDT  
HSTVINK1CEPKAVENSMKFPLQFSA1EAVNEAVTKGPKKRR  
ENMNLKGQ1EAVKEVKEFTDEEKKDMQE1TEOEGFBVNGE1B  
QY1NS1ELIA1KAVGNLND1E1KGHTA1F1DSVGSMSTMSGGAA  
KKYGSVRTCLCBAVLGLVMKORCEKSSFY1FSSPSOCNCY1L  
EVLPDGLSRPMQK1LQKXGKLGGDFTF1EC1DWT1KNTV1H  
DNTV1LSMDM1AEGYSDINVRGSS1NS1IKYKDEDVNP1KI1FA  
FDLVEGQYGC1LNLGEFNNENNY1K1FGMSDSILKF1SIKQGGAM  
VE1VKNP1ALQ1KQGOK

FIG. 20

MSRRNKKQEPQAPIGNETLNFVLDLVEYKSSQEEHYYTQQQOII  
EDELLKLKFKQDODGSNSDDDEBNENNSKQOLLELRVNNIOKQ  
OQVLKIVKGVEKVKDLNLNEKDKNQSSQVEKEORLTTEEE  
VQXVQNLVFNMDYQOLDLNESGHRRERTDYDTEKFVPSHDQ  
KNVYSIYANQYTSQCYWLKVDPYNNVHNSLNRLETAEFPY  
AFPDFFSQTQ1LKTLSNTVYDFTVNDNMLCILARFLLSLERF  
NLIIRNRSSTYRNQNKFGELLETTVPPFVSHRHLQHLOQV  
CEAOPLVNSSLSSOLSKVGSLOVSYPSDTLKLVDTNVKYDQPK  
LQEPPHDFVHSSQAGPVATNAVENNLVLLKVGKHANLNV1S1  
TOFNPDPYVHNLQHLEFGLPELNPTQKQLLENLLSTSKSQH  
KPLRNLNTVYQATVQESRKTQIQLQATIKNNKNQNEETBTKH  
BTSPSTSGMFKEHDLSELTLEDVSNNQATOBYEDSLHKL1L  
RSTNKLTKFLSYKEMEKSMDTFID1LKNYETYNNLRCVSNN  
SPNPHISYELNTDSTPKFLTLNQLOHAKYTPKNEQEFQNT  
NNSKAKISSLSSLESLEDISLCKTASCKNLQNVN1SILSNP  
NICKONPKNPLKHFQCPOLNLNENNSINLDLHNLINS1SEF  
LNENKKIKAFPLKRYQQYLQYDFTKFLTQOLQDQYDQFV  
OLELTTSEVIKWHQWENH1QKQYDFTYBCLPECIKESSQTLQID  
ONTVSDS1KDKL1S1LESIESEKHYTHLNRPSQSSSLIENEI  
ELLACKDCEGKVLYWVYKPKLCPGTQYDYNDSRW

FIG. 22

MKL1FEPFTQPLDCLLIDLQLGTSKNTVADNENLKGCHGGNLDLEIITTCFGPKA  
PNPSKRLA1CPLDLSKNTVADNENLKGCHGGNLDLEIITTCFGPKA  
ARNEDDVNNSLFCFSHANVNTLLKGAAWNKMPHSLVGTYAFV DLL  
NTTYVQFNGQFFTQIVGNCRNEPHLPKPKWVQRS SSSATQAQ  
QLTEPVTQNKFLHNLINNSSSPFYSSSNTQKLDLREAP  
IPTFTNLV1KPIQKLRVNRNLTQKLQKLRRHHKRNQVLSNLSNCPP  
EVFTLDSLHSLRSQSPKERVLKPI IIVLQKLQLOPEMGS KKNKG  
IIKNNLQKQKLSLPLNGLYQPPFDSSLKLLRDKFWI FDSI WTPK  
NENLNQLQALICPISWFLRQIPLKIQTTFYCTEISSTVTFV  
HDWTNKLTT PTFIVF EYKTYL VENNCRHNRSNHNNS KMR  
IPKSNNSREPRI A IPI CRGADEEB TTYI KEHNNKAQIPTQK LIE  
LNRKNTPSFTK1YQSP TQADIREKFKQRLLKKFNNVLELY FMR  
FDFTKSYCDS I PRMECMRILKDAD KNEENGFPVRSQYFNTN'JGV  
KLNFNVNSASRPVKEPYLIDVNRTVHLNSD01VNEEMI FKTAA  
LWEDVKYTCIREDLGFLQGSSLSAPIVLDYLVDDLFYSEKFQKASPS  
QDTL1KLQADDFL1I STDQQV0 IN1XKLAMGGQPKQYANAKRD  
ILAVSSQSSDVTI YQCPAMHI FVKELEWBVKHSTSMMNPYHFRSKS  
SKG1 FRTSLI SLSRQYKQH1TDTLNLSNTVLMQD1HVNWKNISE  
CYSKAFPKDLIS NTV1QNMQRYQPKSFPLR1 IEMTVS CPGC ITKCDPLI  
YEVRFTI LNLNGFLBLSNSNTSKPKDN1 ILLRKSIQHQLQAYIYT  
HIVN.

FIG. 23

1 tcaatactat taattaataa ataaaaaaaaa gcaaaactaca aaaaaaatgt caaggcgta  
 61 ctaaaaaaaag ccataggcctc ctataggcaa tgaaacaaat ctigatttg tattacaaaa  
 121 tctagaagt tacaaaaaccg agttggaca ttataaagcc tagtagtaat agatccaaa  
 181 ggaggatctc aagctttttaa aacttcaaaaa tttaaaggat gatggaaact ctggcaacg  
 241 tggatgtatg gaaagaaaaa actcaataaa ataaaaaaag ttatthaaggaa gactcaatta  
 301 gattaagtag caagtttaat tgataaaaaa agttggctc aaggtagaga aagattgaa  
 361 ttgaacggaa gatgaaacca aaagaatgg actttctgaa tagaaagtga aagagggta  
 421 attaaagaacg attactgaa aataggttaa ttatthaataa ttatgttta acatggacta  
 481 coagttagat tttaatggaa gtggggccca tagaaagcac aagaagaaaa cagatgtatg  
 541 tactgaaaaat tggttggaa ttatccatgc ccaaaaaaaa ttatgtatcaa tttagccaa  
 601 cttaaaagaca tcataatgtt gggttgcattt agatattttt aataaaaaaca attatgtatc  
 661 ttttaatgtg aogatcaact tactgaaaaaa tgagccgca ttctatgcct ttatgtatt  
 721 ttccaaaaacaa atcaaaatcc ttatcaatcc ttatgactg gttaatcatag acgttaattt  
 781 tgataaaat atcttgtatcc ttccatgtatc tagattttta ttatccatgt aagattccaa  
 841 tatttttgaat ataaatgtt ctatccaaacg aatttttttt aattttggaa aaattttgtga  
 901 gatatctgaa atatcttgc cttgtttttt ttccatccgc cacttacaaag gattttttt  
 961 acaaggatct tcggagggct ttatcaatattt agttactcc tcatcataaa tttaggttta  
 1021 agatgtatca ttataggat actttttctc tacacactt aatattgtt acactaaacaa  
 1081 agtccaaatg tattttttt tttatataaagc attccctgtt ttgactcatg taatgtatg  
 1141 ggctatcccc ttatgttgc cttaacgcgtt aatgttttca ttttttttttttttttttt  
 1201 caaggatgtc atctttttt tagttttttt cccttacccaa ttcaatttttt attttttttt  
 1261 tggttaattttaa taacatttgc aattttttttt tagttttttt ttgtttttttt ttttttttt  
 1321 aaaggatggaa atctttttt tagttttttt aatataaaaaa aatctttttt ttttttttt  
 1381 aaaccttttc acctacgtt cttaaagaaaaa cttccaaaaaa aatctttttt ttttttttt  
 1441 aacatcaaaat atctttttt aatataaaaaa aatctttttt tttttttttt ttttttttt  
 1501 aactccaaacg gaaaggcccccc ttgtttttttt ttgtttttttt tttttttttt ttttttttt  
 1561 gttttttttttt ttatgtatgc ttatgtatgc ttatgtatgc ttatgtatgc ttatgtatgc  
 1621 atctt  
 1681 aaaggatggaa atggatcacat ttatcatgtt ttatcatgtt ttatcatgtt ttatcatgtt  
 1741 taaaaggatgc totgttt  
 1801 taaaaggatctt acttt  
 1861 gtatactttt aattt  
 1921 ttctctcatat gaagatgtatgc aatgttttttttttttttttttttttttttttttttttttt  
 1981 aaattt  
 2041 ttcttt  
 2101 aaatgtatctc atcaactgtt ttcttt  
 2161 agaaaaaaat aaaaatataat aagcatccatc ttggaaaaaaa ttttttttttttttttttt  
 2221 ttcttgattttt acttt  
 2281 cattaattttt acaatt  
 2341 ccacaaggaa aaaaatggatcc atgttttttttttttttttttttttttttttttttttttt  
 2401 cccttt  
 2461 aagatctata ttctgtatgc agttatccatc ttatgtatgc ttatgtatgc ttatgtatgc  
 2521 cagttt  
 2581 aggttt  
 2641 cgatttataat ttcatatgtatgc ttatgtatgc ttatgtatgc ttatgtatgc ttatgtatgc  
 2701 tgaatatttttcc ttgttt  
 2761 atatatttttta gtt  
 2821 aaaaaatccg

FIG. 21

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Oxytricha  
EuplotesLCVSYISSLSSFYANLEENALQFLRKESMDPEKPTNLLMRLT  
LCVSSILSSFYATLEESSILGFLRDESMNPENPNVNLLMRLT

FIG. 24

ATTTATACTCATGAAAATCTTATTGAGTTCATTCAGAACAGCTTGACATTGATCTACA  
 GACCAACAGTACTTACAAGAAAATTAAATGTGGTCACTTCATGGCTCGATGAAAAT  
 TCTAFACTACTGTGTTCCGACTACCAAATTAAAGAAAATAGCATTACCATGCCTTCCTGG  
 TGACTTAAAGCCAAACAGCTCATGGTCACTTCATGGCTCGATGAAAAT  
 ATACAACAAACGTAACATTTGGCTATAAAATAGCTAGAAAATGAAGATGTCAACAATAG  
 TCTTTTGTGTCATGGCTTGAGTACTGGTAAAGGGCTGCTGGAAAAT  
 GTTCCACAGTGTGGTGTGCGTACATACGCTTGTGATGTTAATGATCAATTACAGATAAT  
 TCAATTAAATGGGCACTGGTGTGAGTACAGATGTAACGAACTCTCATCT  
 GCGGCCCCAAATGGTGTGCGTACATCTCATCTCATCTCGCAACTGCTGCCAATCAAACAA  
 ACTTACAGAACAGTACACAATTAAACAAATTCTTACACAGCTCAATAATTAAATCTCTTC  
 TTTTTTCTTATAGCAAGATCTCTTCTCATCATCTCATCTAAAGACTAACTGACTTT  
 GAGAGAAAGCTATTTCCTCCAAATTGGTTAAATTCCTCAGAGACTAAAGGTAGGAAT  
 TAATTAAAGGAGTACATGGCTTGTGAAATTATTCATGTTGAGTGTGCTTGTGTT  
 GAATAGTATTGTGCCACCATGGAGGACCGTATTGGACTTGTGCTTGTGAGTAGGCA  
 ATCACCAAAAGGAACGAGTCTGGAAATTATTCATGTTTACAGAAAGTTTACCCCA  
 AGAAATGTTGGCTCAAGAAAATTATCAGAATCTAAATTCTTATT  
 AAGTTTACCCCTTAAATGGTTATTGACATTTCATGGTGTGAAAAAGGTTAAAGGTTAA  
 GGATTTCGGTGTGTTCATTTCTGATATTGGTCACTTCAAGCACAAATTGAAAATT  
 GAATATTGTTGGCAGTGTGTTCATTTCTGCTTATAGCAACATTCTCCAAATTAT  
 ACAGACTTTTTACTGCAACAAATTCTCTCATGCAATTGGTTACTTACAGACA  
 TGAACTTGGAAATAACTTATCACCCCTTATCTGTAAGAATATTAAAGACGTACTTAGT  
 CGAAAGTGTGAGTACATGGTGTGAACTTACAGCTGCTTGTGCAATTCTACATAGCAA  
 AATGGAGGAAITATCACAAAAAAAGCTAATATGAGTTCAAGGTTAGGATCTGGCATCCATCGAC  
 AGGGCGACGCGAAGAAGAAATTCAAAATTAAAGGAGAATCACAAAAAGCTGATCTCCAGCC  
 CACTCAAAAATTTCAGAATCTTCAAGAACAAAGGCCGACTAGTTTACTAAATA  
 TTCTCCAACCCAAATTACTGGCTACCTCAAAAGTAACTGAGCTTAAAGGAAATT  
 GAATATTGTTCTACAGACTTTTCTGATGAAATTCTCTGCTTATAGCAACATTCTCCAAATTAT  
 ACATACCAAAAGGATGGAAATGATGGAGAATCTCAAGGAGTCTGGCTTAAAGGAAATT  
 TTTCGTTAGATCTCAATTCTCAACCAAACTGAGCTTACAGGTGTGAGTTTAAAGGTT  
 TGTTAACGGTACAGCAGAGTACCAAAACCTTATGAGCTTACATAGATAATGTTGAGGACGGT  
 TCATTATCAAATCAGGATGTTATAAGAGATGGAAATATTAAAACAGCTTT  
 GTGGGGTGAAGATACTGCTACATTAGAGAAGATGGTTTTTCTAGGGCTCTAGTTTATC  
 TGCTCCGGATCGTTGATTGGTGTGACGATCTTCTGGAGTTTATAGCGAGTTTAAAGC  
 CAGTCTTACAGGACACCTTAAATTAAACCTGGCTGACGATTCTTATAATCACAC  
 AGACCAACAGCAAGTGTCAATACTCAAAAAGCTGTCATGGCGGATTTCAAAATATAA  
 TCGGAAGGCAATAGAGACAAAATTGGCTGAACTGCTTCAACATGAGTGTGATACGGT  
 TATTCAATTGGTGCATGCACTATTTGTTAAAGAATTGGAAAGTTGGAAACATTCAAG  
 CACAAATGAAATAATTCTCATTCCTGCAAAATTCTGTTAAAGGATATTTCGAAGGTTAA  
 AGGGCTTTAACACTAGAAATCTTATAAAACATTGACACAAATTAAATCAACAAA  
 CACCGTCTCATGCAAAATTGATCATGGTAAAGAACATTTCGGAATGTTATAATCTGC  
 TTTTAAGGATCTATCAATTAAATGTTAGCAGGAAATATGCAATTCTGTTCTACAAAC  
 CATCATGAAATGACAGTCAGCAGCGTTGTCACAAATTACGAAATGATCCTTAAATCGAGT  
 TGAGGTACGATTCACTTATGAACTGGATTGGAAAGCTTATCTCAACACATCTCAA  
 ATTAAAGATAATATCATTCTTGTGAGAAAGGAAATTCAACACTTGCAGC

FIG. 26

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	human	tez1	EST2	p123	Motif 0
	ISLEIENLIGERSNAKMCGLSDFERKROIPEAETIYLNNSFLIPILQSFVTESSDLENR LKDFRNUFSTD--TWEPKNEFNENALACIISNLPRQLPKICQPFYCEIISTUTT- TRELSM沃QET-SANGHYYDFHEN-IVLNKLRLTIEDLVSLRUFFVTEQOQSTSK	AKFHLWANSVVYVLLSFFPVYTBTFQRNR AKFHLWANSVVYVLLSFFPVYTBTFQRNR			
					*****
					*
	human	tez1	EST2	p123	Motif 1
	LFFYRKSVWSKLQSIGIRQHLKRVOLRDVEAEVQHREARPALLTSRLRFTRPKD- TVIFRDKIWLLCRLPFLF1-KCNNEFEKCNENENRDIQK-TTF IVYFRIDTWNKLITPFLF1IVEFKTYLVEVNCFENENRNTLS--NFMNSKORLTPKCSNEF TYYKRNDIMVIMKNS-AJDKETLAEVQEKEVWKS-LGTAPOCRRLTPKK--TTF				
					*****
					*
	human	tez1	EST2	p123	Motif 2
	RPTVNDYVGARTPRERKAERUTSRVIALF-SVAYERA RLITIN-LRKFLIKNGSNKOMLYSTQTLRPAISLKHLINEESSGIPNLLEVYMKLTF RITAIPRGADEEETTYKENEHNKAQPOKLEYRNKSTSTSKLYSEPTOJARIKEF RPTMTENKTKVNSDRKTYKPLTTNTKLNSHLMLKTKN-RMFKEPFGFAVENYDDVPMCKY				
					*****
					*
	human	tez1	EST2	p123	Motif 3 (A)
	KDOLLKHMFGK-KKYFVRDIDKSCYDRKQDLMFRVKK-KLADPEFVIRKXATHATHS KORLAKKENNULPELYMKEDVSCDSPRBCKMRILKD-ALMNENGGRPSOSYFENTN EEFCRMKOWGOPLKFFPATDIEKCIDSVARBLSTFLKTRLLSSDFWINTAQILLKRN				
					*****
					*

FIG. 25

AKFLHWLMSVYVVELRSFFYVTETTFQKNRLFFYRKSWSKLQSIGIRQHLKR  
VQLRDVSEAEVRQHREARPALLTSRLRFIPKPDGLRPIVNMVDYVGARTFRREK  
RAERLTSRVKALFSVLNYERA

FIG. 27

GCCAAGTCTGCACGGCTGATGAGTGTGTA CGTCGTCGAGCTGCTCAGGTC  
TTCTCTTATGTCAGCGAACGACAGCTTTCAAAAGAACAGGCTTTCTAC  
GGAAAGAGTGTCTGGAGCAACTGCAAGCATTTGAATCAGACAGCACTTGAG  
AGGGTGCAGCTGCGGAGCAGCTGCGGAGCAGGGTCAAGCAGCATGGGAAGC  
CAGGGCCGCCCTGCTGACGCTCAGACTCCGCTTCATCCCAAAGCTCGACGGGC  
TGCGGCCATTGAGCATGAGCTACGTCGTTGGAGGCCAGAACGTTCCCGAGA  
GAAAAGAGGGCGAGCCTCTCACCTCGAGGGTAAGGCACGTGTCAGCTGCT  
CAACTACGAGCGGGCGG

FIG. 28

MTEHHTPKSRLRFLRLENQYVYLCTLNDYVQLVLRGSPASSYSNICERLRS  
DVTSFISFLHSTVVGFDSPKDEGVQFSSPKCSQSELAVVVKQMPDFE  
RRRNLLMKGFSMNHDFRAHMHVNGVQNDLVSTF  
PNVLISILESKNWQLLIEIIGSDAMHYILSCKSIPEALPN  
DNYLQISGIPLFPKNNVFEETVSKKRKR  
TIETSITQNKSARKEVSWNSISISRFISIYRSSYKKFKQDLYN  
LNLHSICDRTNTVHMWLQNWIFPRQFG  
LINAQVKQLHKV1PLVSQSTVPPKRLLKVPPLIEQTA  
KRLHRISLSKVYNHYCPYIDTHDDEKILS  
YSLKPNVFAFLRSILVRVPKLIWGNQRIPEIILKD  
LETFKLXSLRYESFSLRYLMSNIKISEI  
EWLVLGKRSNAKMCLSDPEKRKQIAFABFYI  
WLYNSFIIPILOQSFYITESSDLRNR  
TVYFRKDIWKLLCR  
PFTSMKMEA  
PEKINENNVRMDTQKTTLP  
PAVIRLLPKKNTFRLI  
TNLRKRFLIKMG  
GSNKMLVSTN  
QTLP  
RVA  
SILKH  
LINE  
ESSG  
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YMKL  
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FKD  
LL  
KHM  
FGR  
KKY  
FVR  
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KSC  
YDR  
I  
QDLM  
FRI  
VKKL  
KDP  
EFV  
IRKY  
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NFV  
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FIG. 29

FIG. 30

FIG. 30  
(CONTINUED)

EST2	pep	Euplotes	pep	Trans of tetrahymen	Consensus	FFY.TE. .S.YYRK. IN. .-KL. .-.-.F. .K .-.-.V. .-	50
EST2	pep	Euplotes	pep	Trans of tetrahymen	Consensus	NVCRNNS- KEVEKKRL- KIQEENNS- K. E. .-.-.	79 78 92 100
EST2	pep	Euplotes	pep	Trans of tetrahymen	Consensus	TSNNSNNH RUEFENNE FRIEFLPCRG --GPAFKGS RUEPKRPT-- SPPQPKQPSK-- F. GNL SUPLPKM. --	43 44 44 44
EST2	pep	Euplotes	pep	Trans of tetrahymen	Consensus	KEVKEENNS- KVEEKLIPED OLIVNLQILDS- K. K LN.N..L..S	129 120 130 150
EST2	pep	Euplotes	pep	Trans of tetrahymen	Consensus	ADEEFTYK ENKHNIAOPT OKLEYEANK RETSFETKLYS PTOADRIKS IYNSDKRTY LTCTNTKLANS HUMLTAKT- DMFK -DGPFAVEN DQKRNK-- LALNQNLIDS QLVNLTAKD- .Q.L..LNK- .-.. .-.. .-.. .-..	157 158 158 186
EST2	pep	Euplotes	pep	Trans of tetrahymen	Consensus	FQBLINNEN NVL-.-. YD-DVURK EFCVKWKH NK-OISSLRKA QFIEPVYHL RCPJFPMTD IRCEYD .K. .-XKF. .F. .KWK. .G .P. .LFF. T.D .-.. CYD	157 158 158 186

FIG. 31

S-1: FFY VTE TTF QKN RLF FYR KSV WSK  
 S-2: ROH LKR VQL RDV SEA EVR QHR EA  
 S-3: ART FRR EKR AER LTS RVK ALF SVL NYE

A-1: AKF LHW LMS VYV VEL LRS FFY VTE TTF Q  
 A-2: LFF YRK SVW SKL QSI GIR QHL KRV QLR DVS  
 A-3: PAL LTS RLR FIP KPD GLR PIV NMD YVV

FIG. 32

RECORDED BY: GUY A. VAN DER

Poly 4

5'-	t	a	a	g	c	c	t	c	g
	cag	acc	aaa	gga	att	cca	taa	gg	-3'
	Q	T	K	G	I	P	Q	G	

4 (B')

## 5 (c')

3'-	D	D	Y	L	L	I	T
	ctg	ctg	atg	gag	gag	tag	tgg
	a	a	a	a	a	a	
			t	t	t	t	
				c	c		

Poly 1

FIG. 34

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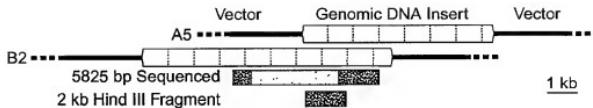


FIG. 33A

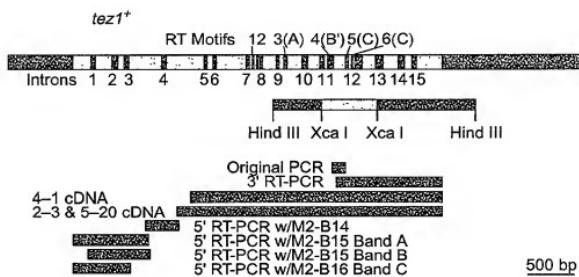


FIG. 33B

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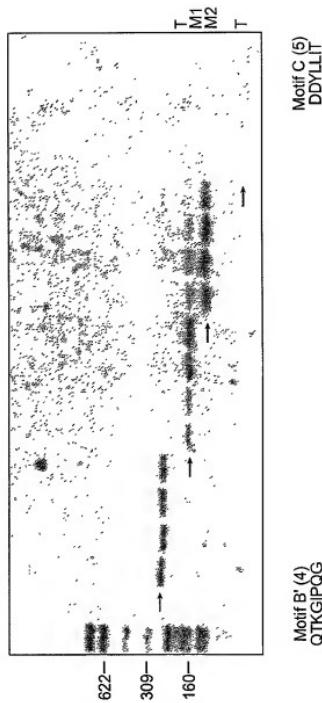


FIG. 35

SC_p103	DGLFOSSASATIVDLYDDILEYSSIFKAFSP-----QDTLKLAKDAFLIS .....
SP_M2	SILSSLFCHYMTTLEDEYLISFTK-----GSVLLRVV
PA_p123	KGIPOOLCVTSYLSFYAALEENAOFLRKSEEMDPEKEETNLMLRLT
Ot	LCVTSYLSFYAALEENAOFLRKSEEMDPEKEETNLMLRLT

Q K V G I P Q G  
caa aaa qtt ggt atc cct cag gg..... <---Actual Genomic Sequence.

FIG. 36

GAA GAT TTG ATT GAT GAA TAC CTA TCG TTT ACG AAA AAG AAA GGA TCA GTG TGT TTA CGA  
 CTT CTA AAC TAA CTA CTT ATG GAT AGC AAA TGC TTT TTC AAC ATG CAC AAC AAT GCT  
 E D L I D B Y L S F T K K G S V L L R

GTA GTC gac gac tac ctc ctc atc acc  
 CAT CTG CTG CTG atg gag gag tag tag  
 V V D D Y L L I T  
 <----- CTG CTG ATG gag gag tag tag  
 a a a a a a a a  
 a a a a a a a a  
 t t t t t t t t  
 C C  
Poly 1

.....gac gat ttc ctc ttt ata aca..... <---Actual Genomic Sequence  
 D D F L P I T

*FIG. 36*  
(CONTINUED)

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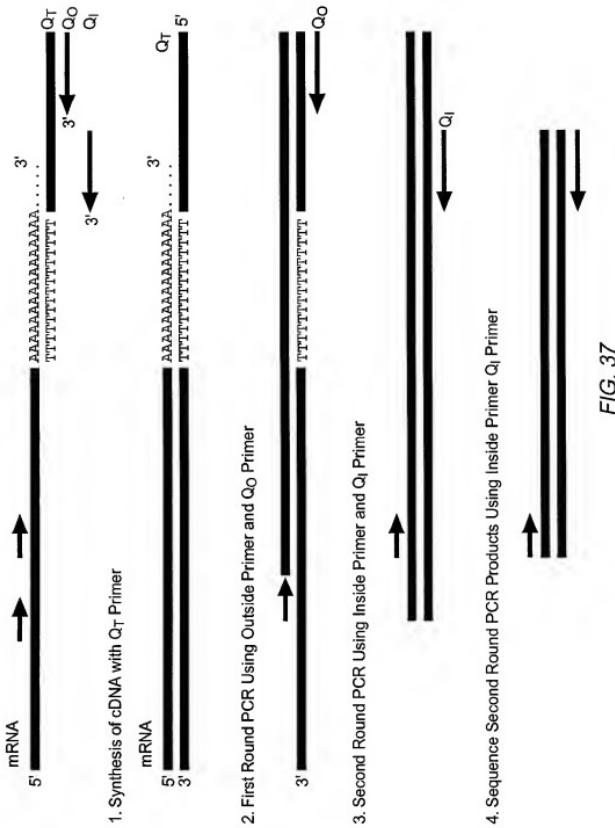


FIG. 37

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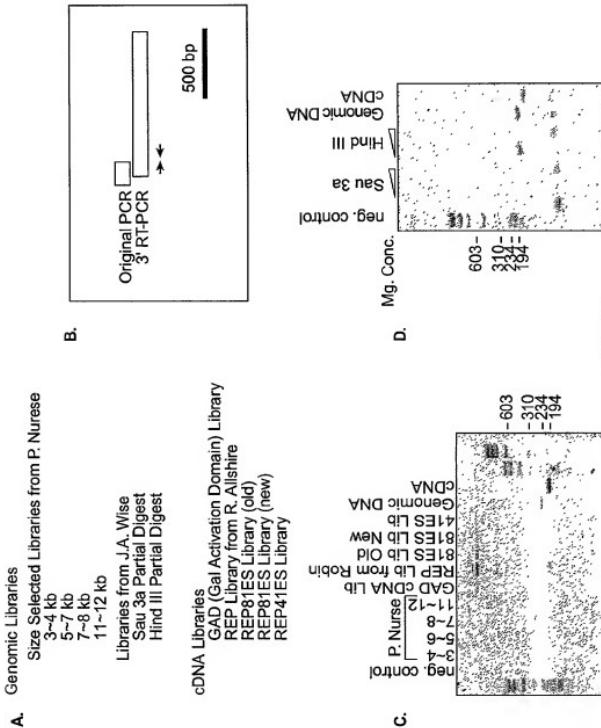


FIG. 38

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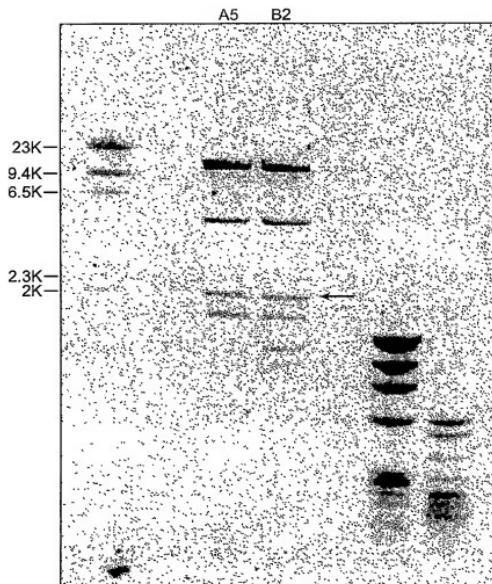


FIG. 39

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J.00354295 : 0441102

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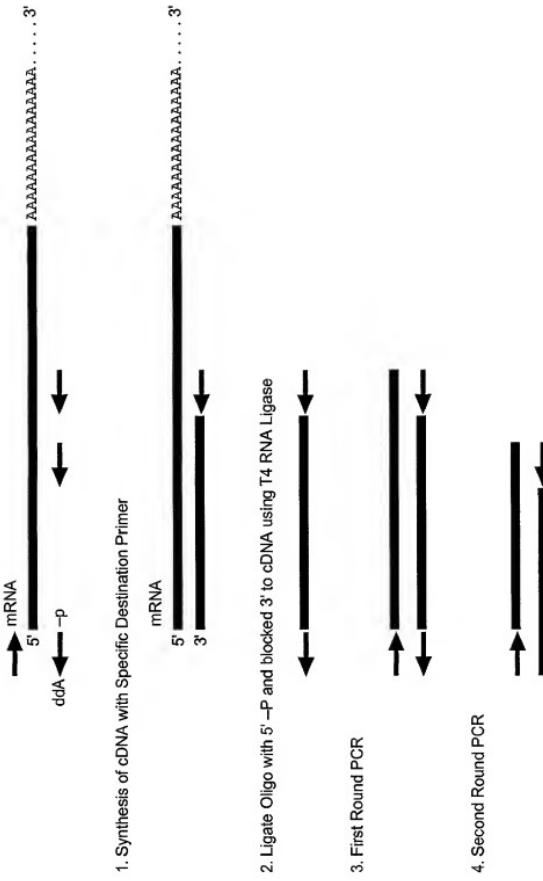


FIG. 40

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S.P.	Tez1p	(429)	WLYNSFLIPILQOSFEVITTSSSDILNRTNEYFKEIDIN	..(35)...	Motif O
S.C.	Bst2p	(366)	WLFLQLQPKIQTIFCIEUSSSTVLTIVFEDHTW	..(35)...	
E.A.	P123	(441)	WIFEDLVSLRCLVEQTEQKSYSYKTVN...*	..(35)...	
*	*	*	*	*	*
S.P.	Tez1p		Motif 1	Motif 2	K
S.C.	Bst2p		p hh b K	b h R	
E.A.	P123		AUTLILKK-->TEFLILTN-LIKR	..(61)...	
*	*	*	GKURLILKK-->TEFRPMTENKKV	..(61)...	
S.P.	Tez1p		Motif 3 (A)	AF	
S.C.	Bst2p		h bhd	GY h	
E.A.	P123		KERFLRDIDKISKSCQDMLRIVK	..(89)...	
*	*	*	ELYTFMRDVSQSDSFIRMECRILK	..(75)...	
*	*	*	YKFLPATMDFGTYNSVREKLSTFLK	..(107)...	
S.P.	Tez1p		Motif 4 (B')	PP hh	h
S.C.	Bst2p		YLQRKVGPQSSITLSFCIFYMDDLDYLSF	..(6)...	
E.A.	P123		YIREGLDFQFQSSILAPVFLVDTDLLETFSEF	..(8)...	
*	*	*	YKQTKGIPQGLCYSSISFTATLLESSLGF	..(14)...	
S.P.	Tez1p		Motif 5 (C)	Y	Motif 6 (D)
S.C.	Bst2p		PDhhb	Gh h	ck h
E.A.	P123		VLLRVRDFLFTIVNKDAKKFLNLSLRGEEFHNTSSTEKTIVNENS	..(1)...	
*	*	*	LIIKLAADFLLTIDQOVTNTKLAMGFOQYNKNAH	..(1)...	
S.P.	Tez1p		LLMFLTDLTITQENAVLFTIEKLINVSRENGFKMNLQTSPLS	..(1)...	
S.C.	Bst2p		*	*	*
E.A.	P123		*	*	*

FIG. 41

A.

Sp_Tip1p	1	- - - - -	M T E H H T P K S R I L R F L E N Q Y V Y L C T	24
Sc_Est2p	1	- - - - -	M E V D V D N Q A D N H G I H S A L K T C E E I K E A K T I L Y S W	33
Ea_p123	1	M E V D V D N Q A D N H G I H S A L K T C E E I K E A K T I L Y S W	33	
Sp_Tip1p	25	L N D Y V Q L V L R G S P A S S Y S N I C E R   R S D V Q T S F S	57	
Sc_Est2p	8	I Q D K L D I D I D Q T N - I S T Y K - - E N L K C G H F N G L D	35	
Ea_p123	34	I Q D K L D I D I D Q T N - I S T Y K - - E N L K C G H F N G L D	35	
Sp_Tip1p	58	I F [ H S T V V G F D S K P D E G V Q F S S P K C S Q S I E L I A N	90	
Sc_Est2p	36	E I L T C F A L P N S R - K I A L P C L P G D L S H K A Y I D H	67	
Ea_p123	62	E I L T C F A L P N S R - K I A L P C L P G D L S H K A Y I D H	67	
Sp_Tip1p	91	V V K Q M F D E S F E R R R - N L L M K G E S M M H E D F R A M H	122	
Sc_Est2p	68	C I Y L L T G E L Y N - N V L T F G Y K I A R N E D - - -	83	
Ea_p123	95	C I Y L L T G E L Y N - N V L T F G Y K I A R N E D - - -	83	
Sp_Tip1p	123	V N G V Q N D L V S T F P N Y L I S I L E S K N W Q L L E I L G	155	
Sc_Est2p	94	- - - V N N S L F C H S A I N V N V T L L K G A A W K M F H S L V G	123	
Ea_p123	123	- - - V N N S L F C H S A I N V N V T L L K G A A W K M F H S L V G	123	
Sp_Tip1p	156	S D A M H Y L L S K G S I F E A L P N D N Y L Q I S G L P L E F K N	188	
Sc_Est2p	124	T Y A F V D L L I N Y T V I Q F N - G Q F F T Q I V G N R C N E P	156	
Ea_p123	153	T Y A F V D L L I N Y T V I Q F N - G Q F F T Q I V G N R C N E P	156	
Sp_Tip1p	189	N V F E E T V S K K R K R T I E I S T Q N - - K S A R K E V S	218	
Sc_Est2p	156	H L P P K W V Q - R S S S S A T A A Q I - - K Q L T E P V T	183	
Ea_p123	186	H L P P K W V Q - R S S S S A T A A Q I - - K Q L T E P V T	183	
		L K V N D K F D K - K Q K G G A A D M N E P R C C S T C K Y N V K	217	

A.	Sp_Tip1p	219	WNSISISRFSSIFYRSSYYKKFKQDLYFNLHSSLCD	251
Sc_Est1p	184	N-----DHFLNNNNNVPWNWNMKMSRTRL	200	
Ea_p123	218	NEK-----	248	
Sp_Tip1p	252	RNTVHMWLQWIEPRQFGLINAFOQVKQQLHKVPL	284	
Sc_Est1p	201	-----YSKLPLPSSS-----	273	
Ea_p123	249	R-----NNQFLKEKKHFVSNKNNSAMDRAGT	275	
Sp_Tip1p	285	V-----QSITYVVPKRLKKVYPLIEQTAKRLHRS	313	
Sc_Est1p	224	TNT-----LVKTPQRLLKVRINLTQKLLKRLN	313	
Ea_p123	276	FTNIFRFRNRIRKKLKDVKYEKIAYMLEKVKDFN	308	
Sp_Tip1p	314	LSKVYVNHYCPTYIDTHDEKILSYSLKPNA	342	
Sc_Est1p	253	YVSILNSICPPLEGTVLDLSHLSRQSPKER	282	
Ea_p123	309	FNYYLTKSCPLPENWRERKQKIEENLNKTEREEK	341	
Sp_Tip1p	343	-----VFAFLRSITLVRVFPKL	359	
Sc_Est1p	283	-----VLFKIVVLLQKLLPQE	289	
Ea_p123	342	SKYYEEELFSYTDDNKCVTQFENEFFYNILPKDF	374	
Sp_Tip1p	360	WGQNQRILFEIILKDKDLTEFLKLSRYESFSLHYLMS	382	
Sc_Est1p	300	FGSKNGKQKLNKLNLLSPLHNGYLPHDPSL	332	
Ea_p123	375	LTKRNLKFQKVVVYELNKHNLKLLK	406	
Sp_Tip1p	393	NIKISEIIEWLVLGKRSNAKMCSDFELKRKQI	425	
Sc_Est1p	333	KLRLKDFRWLFISS-----DIWFTHNFENLNQI	425	
Ea_p123	407	KINTREISWMQVETS-AKHFYYFDHEN-IVLVW	437	

FIG. 42  
(CONTINUED)

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Sp_Tip1p	426	E F I Y W L Y N S F T I P T L Q S F F Y I T E S S D L R N R T V Y 488	Sp_Est1p	363	C F I S W L F R Q L T K P L I Q T F Y C T I S S T V T - V Y 384	Sc_Est1p	438	K L L R W T I E D L V V S L U R C E F Y V I T E Q Q K S Y S T V Y 470
Sp_Tip1p	459	F R K D T W K L L C R P F I T S M K M E A F E K I N N V R M D 481	Sc_Est1p	395	F R H D T W M N K L T I P F I V E Y E K I Y V E N N V C R H N S 477	Sc_Est1p	471	Y R K N T L W D V I M K W S L A D L K K T E L V Q E K E V E E W 503
Sp_Tip1p	492	T Q K T T L P P A V I R L L P K K - I N T F R L I T N L R K R F L 522	Sc_Est1p	428	Y T L S N F N H S K M R I T P K S S N I E F R I A I P C R G A D 480	Sc_Est1p	471	E a _ p 123 504 K K S L G F A P P G K L R L P K K - T T F R P I M T F N K K I V 534
Sp_Tip1p	523	I K M G S N K K M L V S I N Q T L R P V A S I L K H L I N E - - 552	Sc_Est1p	461	E E E - - F T I Y K E N H K N A Q P T Q K L L E Y L R N K R P T 491	Sc_Est1p	535	N S D - - R K T T K L T T N T K L L N S H L M L K T L K N R - M F 564
Sp_Tip1p	563	E S S G I P F N L E V Y M K L L T F K K D L L K H R M F G R - K K 584	Sc_Est1p	492	S F T K L Y S P T Q I A D R I K E F Q R L L K K F N N V L I P E L 524	Sc_Est1p	565	K D P F G F A V F N Y D D V M K K Y E E F V C K K W Q V G Q P K L L 587
Sp_Tip1p	585	Y F V R I D I K S C Y D R I K Q D D L M F R I V K K K L K D P E - F 616	Sc_Est1p	525	Y F M K F D I V K S C Y D S I P R I M E C M R I L K D A L K N E N G F 557	Sc_Est1p	598	F F A T T M D J E K C Y D S V N R E K L S T F L K T K L L S S D F 630
Sp_Tip1p	617	V L R K Y A T I H A T S D R A T K N - - - - - 634	Sc_Est1p	568	V F R S Q Y F F N T N T G - - - - - 570	Sc_Est1p	631	W I M T A Q I V D S K N F R K K E M K D Y F R Q K 663
Sp_Tip1p	648	- - - - - 666	Sc_Est1p	631	- - - - - 666	Sc_Est1p	631	- - - - - 666

FIG. 42  
(CONTINUED)

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FIG. 42  
(CONTINUED)

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FIG. 42  
(CONTINUED)

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B.	Sp_Tip1p	1	- - - - -	- - - - -	MTEHHHTPKRSRILRFLLENQYVYVLC	24
	Sc_Est2p	1	- - - - -	- - - - -	-MKLFEF	7
	Ea_p123	1	<b>M</b> EV <b>D</b> V <b>D</b> N <b>Q</b> A <b>D</b> N <b>H</b> I <b>S</b> A <b>L</b> K <b>T</b> C <b>E</b> I <b>K</b> E <b>A</b> K <b>T</b> LY <b>S</b> W	33		
Sp_Tip1p	25	LNDYVQLVLRGSPASSNSICERLRSQTSFS	57			
Sc_Est2p	6	QDKLDLQTN - - STYK -- ENLKCGHFNGL	35			
Ea_p123	34	IQKVIRCRNQSQ - - SHYK -- DLEDIKIFQAQN	61			
Sp_Tip1p	58	IFLHSSTVVGFDSPKDEGVQFSSPKCSQSEL	90			
Sc_Est2p	36	EILTTCFALPNSR-KIALPCLPGDLSHKAVID	67			
Ea_p123	62	IVATPRDYNEEDFKVIARKEVFSTGLMIELIDK	94			
Sp_Tip1p	91	VVKQMFD <b>E</b> SFERR - NLLMMKG <b>F</b> SMNHEDFRAMH	122			
Sc_Est2p	68	C-IYLLTGELYN - - NVLTFGYKIARNED	93			
Ea_p123	95	CLVELLSSSDVSDRQKLQCFQQLKGNNQ - - -	122			
Sp_Tip1p	123	VNGVQNDLVSTFPNYLISILESKNWQLLIEIG	155			
Sc_Est2p	94	- - VNNNSLFCHSANVNNTLLKGAAWKMFHSLVY	123			
Ea_p123	123	- - LAKTHLLTALSTQKQYFFQDEWNQVRAMIG	155			
Sp_Tip1p	156	SDAMHY <sub>LL</sub> SKGSI <b>F</b> EALPNDNYLQISIGIPLFKN	186			
Sc_Est2p	124	TYAFVDFL <sub>LL</sub> INYTIQFLFQRTSEGTLVQ	155			
Ea_p123	153	NELFR <sub>LL</sub> YTYYKLLFQRTSEGTLVQFCGNNVNFDH	185			
Sp_Tip1p	189	NVVEFTVSKKRKRTTTSITQN - - KSAKREVS	218			
Sc_Est2p	156	HLPPKWWQ - - SRSSTSATAAQI	155			
Ea_p123	186	KLVNDKFKD - - KQKGGAAADMNEPRCCSTCKYNYVK	217			

FIG. 42  
(CONTINUED)

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FIG. 42  
(CONTINUED)

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B.							
Sp_Tip1p	426	EF I YWL YN S F I I P I L Q S F F Y I T E S S D L R N R T V Y	458				
Sc_Est2p	363	C F I S W L F R Q L I P K I Q T F F Y C T E I S S T V T - I V Y	394				
Ea_p123	438	K L R M I F D L V V S L I R C F F Y V T E Q Q K S Y S K T V Y	470				
Sp_Tip1p	459	<b>F</b> R K D I <b>W</b> K L L C R P F I T S M K M E A F E K I N E N N V R M D	491				
Sc_Est2p	395	<b>F</b> R H D T W N K L I T P F I V E Y F K T Y L V E N N V C R N H N S	427				
Ea_p123	471	<b>Y</b> R K N I <b>W</b> D V I M K M S I A D L K K E T L A E V Q E K E V E E W	503				
Sp_Tip1p	492	T Q K T T L P P A V I R L L P K K - N T F R L I T N L R K R F L	522				
Sc_Est2p	428	Y T L S N F N H S K M R I P K K S - N N E F R I I A I P C R G A D	460				
Ea_p123	504	K K S I G F A P G K L R L I P K K - T T F R P I I M T F N K K I V	534				
Sp_Tip1p	523	I K M G S N K K M L V S T N Q T L R P V A S I [K H] I N E - -	552				
Sc_Est2p	461	EE E - - F T I Y K E N H K N A I Q P T Q K I L E Y L R N K R P T	491				
Ea_p123	535	N S D - - R K T T K L T T N T N K L L N S H L M L K T L K N R - M F	564				
Sp_Tip1p	553	E S S G I P F N L E V Y M K L L T F K K D L L K H R M F G R - K K	584				
Sc_Est2p	492	S F T K I Y S P T Q I A D R I K F Q R L L K K F N N V L P E L	524				
Ea_p123	565	K D P F G F A V F V N Y D D V M K K Y E E F V C K W K Q V G Q P K L	597				
Sp_Tip1p	585	<b>Y</b> F V R I D I K S C Y D R I K Q D L M F R I V K K K L K D P E - F	616				
Sc_Est2p	525	<b>Y</b> F M K F D V K S C Y D S I P R M E C M R I L K D A L K N E G F	557				
Ea_p123	598	<b>F</b> E A T M D I E K C Y D S V N R E K L S T F L K T T K L L S S D F	630				
Sp_Tip1p	617	V I R K Y A T I H A T S D R A T K N - - - - -	634				
Sc_Est2p	558	F V R S Q Y F F N T N G - - - - -	570				
Ea_p123	631	W I M T A Q I L K R K N N I V I D S K N F R K K E M K D Y F R Q K	663				

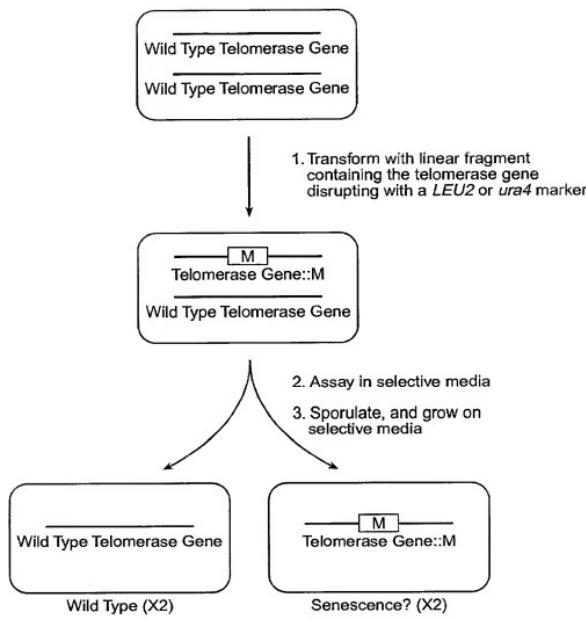
FIG. 42  
(CONTINUED)

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FIG. 42  
(CONTINUED)

B.	Sp_Tip1p	850	<chem>[L][A][S][F][A][Q][V][F][I][D][I][T][H][N][S][K][F][N][S][C][C][N][I][Y][R][L][G][Y][S][M][C][M][R]</chem>	882
	Sc_Est2p	773	<chem>[L][N][S][T][N][T][V][L][M][D][H][V][K][N][I][S][E][G][I][T][T][E][D][F][A][N][K][L][F][I][S][G][Y][K]</chem>	783
	Ea_p123	895		- - -
	Sp_Tip1p	883	<chem>A[Q][A][Y][L][K][R][M][K][D][I][F][P][Q][R][M][F][I][T][D][L][I][N][V][I][G][R][K][W][K][K]</chem>	915
	Sc_Est2p	794	<chem>- - - [Y][K][S][A][F][K][D][L][S][I][N][P][H][S][F][L][Q][R][I][E][M]</chem>	821
	Ea_p123	928	<chem>Y[M][Q][C][A][K][Y][K][D][H][F][K][N][L][A][M][S][M][I][D][L][E][V][S][K][I][Y][S][V]</chem>	960
	Sp_Tip1p	916	<chem>L[A][E][I][L][G][Y][T][S][R][R][F][L][S][A][E][V][K][W][L][F][C][L][G][M][R][D][G][K][P][S]</chem>	948
	Sc_Est2p	822	<chem>T[V][S][G][C][P][I][T][K][C][D][P][L][I][E][Y][E][V][R][F][T][I][L][N][G][F][L][E][S][L][S][S][N]</chem>	864
	Ea_p123	961	<chem>T[R][A][F][F][K][Y][L][V][C][N][I][K][D][T][I][F][G][E][E][H][Y][P][D][F][F][L][S][T][L][K][H][F]</chem>	983
	Sp_Tip1p	949	<chem>F[K][Y][H][P][C][F][E][Q][L][I][Y][Q][F][Q][S][L][T][D][L][I][K][P][L][R][P][V][I][R][Q][V][L][F]</chem>	981
	Sc_Est2p	865	<chem>T[S][T][S][I][I][I][L][R][K][E][I][Q][H][L][Q][A][Y][Y]</chem>	877
	Ea_p123	994	<chem>I[E][F][S][T][K][Y][I][E][N][R][V][C][M][I][L][K][A][K][E][A][K][L][K][S][D][Q][C]</chem>	1022
	Sp_Tip1p	982	<chem>L[H][R][I][A][D][I][Y][H][I][V][N][D]</chem>	988
	Sc_Est2p	878		
	Ea_p123	1024		1031

*FIG. 42*  
(CONTINUED)



(These cells will show a senescence phenotype if the disrupted gene encodes a telomerase subunit.)

FIG. 43

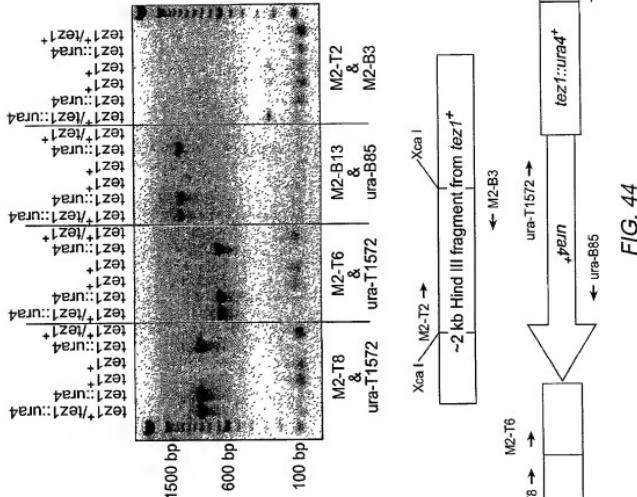


FIG. 44

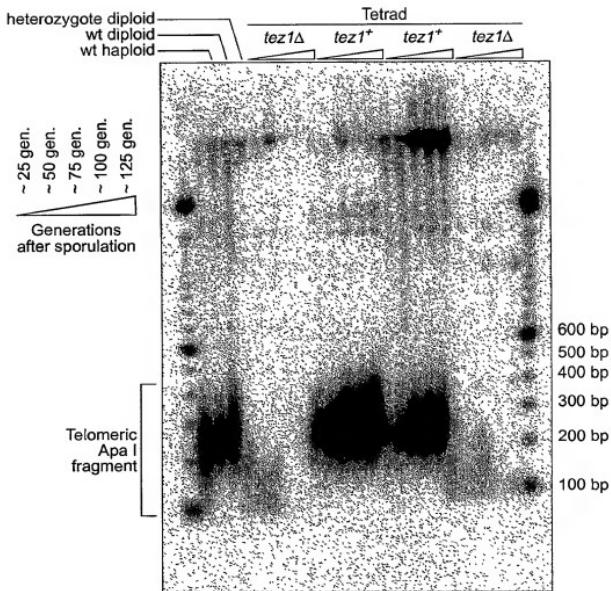


FIG. 45

FIG 46

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FIG. 46  
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FIG. 46  
(CONTINUED)

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33098 tataatacgccggatcttcattttgcagg C GCT AAC AGG TAT TTG CGG ATA GAT ATA 3155  
 582 R K K V F V R D I  
 33156 AAA TCC TGT TAT GAT CGA ATA AAG GAA GAT TTG ATG TTT CGG ATT GTT AAA AAG AAA CTC 3215  
 592 K S C Y D R I K Q D L M P R I V K K K L  
 33211 CCC GAA TTT GTA ATT CGA AGG TAT GCA ACC ATA CAT GCA ACT AGT GAC CGA GCT 3275  
 612 K D P E F V I R Y A T I H A T S D R A  
 33216 AGG TAT GAT CGC TTT GAT CGG TTT GAG GCG TTT GAT TCC TAT T 9aaatgttattttcatggaaattttacaaa 3343  
 612 K D P E F V I R Y A T I H A T S D R A  
 33276 AGA AAA AAC TTT GGT AGT GAG GCG TTT GAT TCC TAT T 9aaatgttattttcatggaaattttacaaa 643  
 632 T K W P S E A F S Y F  
 3344 atcctttttag TT GAT ATG GTG CCT TTG GAA AAA GTC GCG CAG TTA CTT TCT ATG AAA ACA 3405  
 644 D M V P F E K V V Q L L S M K T  
 33406 TCA GAT ACT TTG TTT GGT GAT TTT GTC ACC AAA AGT TCT TCT GAA ATT ATT TTT 3445  
 660 S D T L P V D D Y V K T S S E S I  
 33466 AAA ATG CTC AAC GAA CAT CTC TCT GGA CAC ATT GTT AAG GATaccatgtgaaatataaaaa 3532  
 680 K M L K E H L S G H I V K  
 33333 ctaatggaaactag ATA GGA ATT TCT CAA TAC CTT CAA AAA GTT GGT ATC CCT CAG GCC TCA 3593  
 693 T I G S S Q Y L Q K W G T P Q G S  
 33594 ATT CTG TCA TCT TTT TTG TGT ATT CAT ATT GAA GAT TTG ATT GAT GAA TAC CTA TCG 3653  
 709 I L S P F S L C H F Y M E D L I D E Y L S  
 33654 TTT ACG AAA AGG AAA GGA TCA GTG TTG TTA COA GTP GAC GAT TTC CTC TTT ATA ACA 3713  
 729 F T K K K G S V L L R V D D F I T  
 33744 GTT AAA AGG GAT GCA AAA ATT TTG AAT TTA TCT TTA AGA G 9tagtgtgtgttatcc 3776  
 749 V N K K D A K K P L N L S T S L R G  
 33778 taatgttcataaccctgttgcagg GA TTT GAG AAA AAC CAC ATT ATT TTG AGC AGC CTC GAG AAA ACA GTC 3840  
 765 F P E K H N P S T S L E K T V  
 33841 ATA AAC TTT GAA ATT AGT ATT GGG ATA ATA AAC ATT ACT ATT ATT ATT GAA AGC AGG AAA 3900  
 784 T N P F N P F N P F N P F N E S K A A A A

*FIG. 46*  
(CONTINUED)

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FIG. 46  
(CONTINUED)

*FIG. 46*  
(CONTINUED)

1  
met ser val tyr val val glu leu leu  
GCCAAGTTCTGCCTGGCTG ATG AGT GTG TAC GTC GTC GAG CTG CTC

10  
arg ser phe phe tyr val thr glu thr phe gln lys asn arg  
AGG TCT TTC TTT TAT GTC ACG GAG ACC ACG TTT CAA AAG AAC AGG

30  
leu phe phe tyr arg lys ser val trp ser lys leu gln ser ile  
CTC TTT TTC TAC CGG AAG AGT GTC TGG AGC AAG TTG CAA AGC ATT

40  
gly ile arg gln his leu lys arg val gln leu arg glu leu ser  
GGA ATC AGA CAG CAC TTG AAG AGG GTG CAG CTG CGG GAG CTG TCG

50  
glu ala glu val arg gln his arg glu ala arg pro ala leu leu  
GAA GCA GAG GTC AGG CAG CAT CGG GAA GCC AGG CCC GCC CTG CTG

60  
thr ser arg leu arg phe ile pro lys pro asp gly leu arg pro  
ACG TCC AGA CTC CGC TTC ATC CCC AAG CCT GAC GGG CTG CGG CCG

70  
ile val asn met asp tyr val val gly ala arg thr phe arg arg  
ATT GTG AAC ATG GAC TAC GTC GTG GGA GCC AGA ACG TTC CGC AGA

80  
100  
glu lys ala glu arg leu thr ser arg val lys ala leu phe  
GAA AAG ARG GCC GAG CGT CTC ACC TCG AGG GTG AAG GCA CTG TTC

110  
ser val leu asn tyr glu arg ala arg arg pro gly leu leu gly  
AGC GTG CTC AAC TAC GAG CGG CGC CGG CCC GGC CTC CTG GGC

120  
ala ser val leu gly leu asp asp ile his arg ala trp arg thr  
GCC TCT GTG CTG GGC CTG GAC GAT ATC CAC AGG GCC TGG CGC ACC

130  
150  
phe val leu arg val arg ala gln asp pro pro pro glu leu tyr  
TTC GTG CTG CGT GTG CGG GCC CAG GAC CCG CCT GAG CTG TAC

160  
170  
phe val lys val asp val thr gly ala tyr asp thr ile pro gln  
TTT GTC AAG GTG GAT GTG ACG GGC GCG TAC GAC ACC ATC CCC CAG

180  
asp arg leu thr glu val ile ala ser ile ile lys pro gln asn  
GAC AGG CTC ACG GAG GTC ATC GCC AGC ATC ATC AAA CCC CAG AAC

190  
200  
thr tyr cys val arg arg tyr ala val val gln lys ala ala met  
ACG TAC TGC GTG CGT CGG TAT GCC GTG GTC CAG AAG GCC GCC ATG

FIG. 47

210  
gly thr ser ala arg pro ser arg ala thr ser tyr val gln cys  
GGC ACG TCC GCA AGG CCT TCA AGA GCC ACG TCC TAC GTC CAG TGC

220  
gln gly ile pro gln gly ser ile leu ser thr leu leu cys ser  
CAG GGG ATC CCG CAG GGC TCC ATC CTC TCC ACG CTG CTC TGC AGC

240  
leu cys tyr gly asp met glu asn lys leu phe ala gly ile arg  
CTG TGC TAC GGC GAC ATG GAG AAC AAG CTG TTT GCG GGG ATT CGG

250  
arg asp gly leu leu leu arg leu val asp asp phe leu leu val  
CGG GAC GGG CTG CTC CTG CGT TTG GTG GAT GAT TTC TTG TTG GTG

270  
thr pro his leu thr his ala lys thr phe leu arg thr leu val  
ACA CCT CAC CTC ACC CAC GCG AAA ACC TTC CTC AGG ACC CTG GTC

280  
arg gly val pro glu tyr gly cys val val asn leu arg lys thr  
CGA GGT GTC CCT GAG TAT GGC TGC GTG GTG AAC TTG CGG AAG ACA

300  
val val asn phe pro val glu asp glu ala leu gly qly thr ala  
GTG GTG AAC TTC CCT GTA GAA GAC GAG GCC CTG GGT GGC ACG GCT

310  
phe val gln met pro ala his gly leu phe pro trp cys gly leu  
TTT GTT CAG ATG CCG GCC CAC GGC CTA TTC CCC TGG TGC GGC CTG

330  
leu leu asp thr arg thr leu glu val gln ser asp tyr ser ser  
CTG CTG GAT ACC CGG ACC CTG GAG GTG CAG AGC TAC TCC AGC

340  
tyr ala arg thr ser ile arg ala ser leu thr phe asn arg gly  
TAT GCC CGG ACC TCC ATC AGA GCC AGT CTC ACC TTC AAC CGC GGC

360  
phe lys ala gly arg asn met arg arg lys leu phe gly val leu  
TTC AAG GCT GGG AGG AAC ATG CGT CGC AAA CTC TTT GGG GTC TTG

370  
arg leu lys cys his ser leu phe leu asp leu gln val asn ser  
CGG CTG AAG TGT CAC AGC CTG TTT CTG GAT TTG CAG GTG AAC AGC

390  
leu gln thr val cys thr asn ile tyr lys ile leu leu leu gln  
CTC CAG ACG GTG TGC ACC AAC ATC TAC AAG ATC CTC CTG CTG CAG

400  
ala tyr arg phe his ala cys val leu gln leu pro phe his gln  
GCG TAC AGG TTT CAC GCA TGT GTG CTG CAG CTC CCA TTT CAT CAG

**FIG. 47**  
(CONTINUED)

420

gln val trp lys asn pro his phe ser cys ala ser ser leu thr  
 CAA GTT TGG AAG AAC CCA CAT TTT TCC TGC GCG TCA TCT CTG ACA

440

arg leu pro leu leu leu his pro glu ser gln glu arg arg asp  
 CGG CTC CCT CTG CTA CTC CAT CCT GAA AGC CAA GAA CGC AGG GAT

450

val ala gly gly gln gly arg arg pro ser ala leu arg gly  
 GTC GCT GGG GGC CAA GGG CGC CGC CGG CCC TCT GCC CTC CGA GGC

460

arg ala val ala val pro pro ser ile pro ala gln ala asp ser  
 CGT GCA GTG GCT GTG CCA CCA AGC ATT CCT GCT CAA GCT GAC TCG

480

thr pro cys his leu arg ala thr pro gly val thr gln asp ser  
 ACA CCG TGT CAC CTA CGT GCC ACT CCT GGG GTC ACT CAG GAC AGC

490

pro asp ala ala glu ser glu ala pro gly asp asp ala asp cys  
 CCA GAC GCA GCT GAG GAA GCT CCC GGG GAC GAC GCT GAC TGC

510

pro gly gly arg ser gln pro gly thr ala leu arg leu gln asp  
 CCT GGA GGC CGC AGC CAA CCC GGC ACT GCC CTC AGA CTT CAA GAC

520

his pro gly leu met ala thr arg pro gln pro gly arg glu gln  
 CAT CCT GGA CTG ATG GCC ACC CGC CCA CAG CCA GGC CGA GAG CAG

540

thr pro ala ala leu ser arg arg ala tyr thr ser gln gly gly  
 ACA CCA GCA GCC CTG TCA CGC CGG GCT TAT ACG TCC CAG GGA GGG

550

arg gly gly pro his pro gly leu his arg trp glu ser glu ala  
 AGG GGC GGC CCA CAC CCA GGC CTG CAC CGC TGG GAG TCT GAG GCC

560

OP  
 TGA GTGAGTGTTGGCGAGGCCCTGCATGTCCGGCTGAAGGCTGAGTGTCCGGCTGAGGC  
 CTGAGCGAGTGTCAGCCAAGGGCTGAGTGTCCAGCACACCTGCCTTCACTTCCCCAC  
 AGGCTGGCGTTCGGCCACCCAGGGCCAGCTTCTCACCAGGAGCCGGCTTCCACT  
 CCCCCATAGGAATAGTCATCCCCAGATTGCCATTGTTACCCCTGCCCTGCCCTTCC  
 TTTGCCTTCCACCCCAACATTCAAGGGTGTGCCCTGTACACAGGCAGGACCCCTG  
 AATTTGGAGTGACCAAGGGTGTGCCCTGTACACAGGCAGGACCCCTGACCTGGATGGG  
 GTCCCTGTGGTCAAATTGGGGGAGGTGCTGTGGAGTAAAATCTGAATATATGAGTT  
 TTTCAAGTTTGGAAAAAAAAAAAAAA

**FIG. 47**  
(CONTINUED)

Motif -1							
Ep p123	...LVVSLIRCFYYVTEQQKSYSKT...						
Sp Tez1	...FIPILQSFFYITESSDLRNRT...						
Sc Est2	...LIPKIIQTFYYCTEISSTVTIV...						
Hs TCP1	...YVVELLRSFFYVTETTFQKNRL...						
consensus	FFY TE						
 Motif 0						K	
Ep p123	...KSLGFAPGKLRLIPKKT--TFRPIMTFNKKIV...	p	hhh	K	hR	h	R
Sp Tez1	...QKTTLPAAVIRLLPKKN--TFRLLTNLRKRLF...						
Sc Est2	...TLSNFNHSKMRIIPKKSNNEFRIIAIPCRGAD...						
Hs TCP1	...ARPALLTSRLRFIPKPD--GLRPIVNMDYVVG...				R	PK	I
consensus							
 Motif A						AF	
Ep p123	...PKLFATMDIEKCYDSVNREKLSTFLK...	h	hDh	GY	h		
Sp Tez1	...RKKYFVRIDIKSCYDRIKQDLMFRIVK...						
Sc Est2	...PELYFMKFVDVKSCYDSIPIRMECMRLK...						
Hs TCP1	...PELYFVVKVDVTGAVIDTIPQDRLTEVIA...//...		F	D	YD		
consensus							
 Motif B						hPQG	pS hh
Ep p123	...NGKFKYKQTKGIPPGGLCVSSILSSFYYA...						
Sp Tez1	...GNSQYLOKVGIPQGSILSSFLCHFYME...						
Sc Est2	...EDKCYIREDGGLFQGSSLASAPIVDLVDD...						
Hs TCP1	...RATSYVQCQGIPQGSILSTLLCSCLYG...			G	QG	S	
consensus							
 Motif C						Y	
Ep p123	...PNVNLLMRLLTDYLLITIQENN...	h	F	DD	hhh		
Sp Tez1	...KKGSVLLRVVVDLFLFITVNKKD...						
Sc Est2	...SQDTLILKLADDFLIISTDQQQ...						
Hs TCP1	...RRDGLLLRLVVDPLLVTPHLTH...			DD	L		
consensus							
 Motif D						Gh	h cK
Ep p123	...NVSRENGFKFNMKKL...						
Sp Tez1	...LNLSLRGFEKHNFST...						
Sc Est2	...KKLAMGGFQKYNAKA...						
Hs TCP1	...LRTLVRGVPEYGCVV...						
consensus	G						

FIG. 48

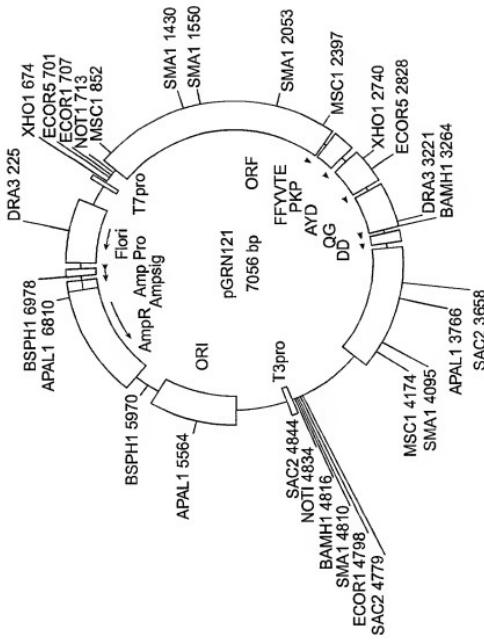


FIG. 49

1 GCAGCGCTGC GTCTCTGCTGC GCACGTGGGA AGCCCTGGCC CGGGCACCC  
 51 CGCGATGCC GCGCGTCCTC CGCTGCCGAG CGTGGCCCTC CCTGCTGCC  
 101 AGCCACTACC GCGAGGTGCT GCGCTGGCC AGTTGCTGC GGCGCTGGG  
 151 GCCCCAGGG TGCGCGCTG TGCAAGCCGG GGACCCGGCG GCTTTCGCG  
 201 CGNTGGCTGC CCANTGCTG TGTCGGCTG CCTGGGANNG ANGCNC  
 251 CCCGGCCCG CTCCTCTCC CGAAGTGTCC TGCCTGAANG ANCTGGTGGC  
 301 CGGAGTGTG CANANGCTG GCGGANCCGG CGGAAANAAC GTGCTGCC  
 351 TCGGCTTGCG GCTGCTGAC GGGGCCCGGG GGGGCCCCCCC CGAGGCC  
 401 ACCACAGCC TGCGCAGCTA CCTGCCAAC ACGGTACCG ACCCACTGCC  
 451 GGGGAGCGGG GCGTGGGGGC TGCTGCTGC CGCGTGGGC GACGACGTG  
 501 TGTTGCTGCTTG CGTCGGCTNT TTGTCGTTGTT GGNTCCAGC  
 551 TGCGCCCTACG ANGTGGCGC GCGCCGCTG TACCACTCC CGCGCTCNAC  
 601 TCAGGGCCGG CCCCGCCAC AGCCTANTGG ACCGAANGC GCTGCGGATC  
 651 CAACGGCCCT GGAAACATCA CGTCAGGGAG GCGGGGGTCC CCTGGGCTG  
 701 CGACGGCCGG GTGCGGAGAG GCGGGGGGAG AGTGGCAGCC GAAGTGTGCC  
 751 GTTGGCCCAAAG AGGCCAGGG TGTCGGCTG CCTTGACCG GACGCC  
 801 CGGTGGCA GGGGCTTGG GCCCACCCGG CGAGGACGCC TGGACCCAGT  
 851 GACCGTGGTT CTGTCGTTG GTCACCTGCC AGACCCGGCG AAAGAAC  
 901 CTCTTGGAG GTGCTGGCTC CGACCGCCCG CCACCTCCAC CCATCGTGG  
 951 GCGCCACCA CGACCGCCCG CCCCATCTCA CATCGGCCG ACCACCTCT  
 1001 GGACACCCCG TTGCTCCCCG GTGACCCCG AGACCAAGCA CCTCCCTAC  
 1051 TCCTCAGGCC ACAAGNACAC TGCGNCCTC TTCCCTACTC AATATATCTG  
 1101 AGGCCAGCC TGACTGGCTG TCGGGAGTT CGTGGAGACA NTCTTTCTGG  
 1151 TTCCAGGCC TGGATGCCAG GATTCCCCG AGTTGCCCG GCTGCC  
 1201 GCGNACTGG CAATGCGGC CCCCTGTTCT GGAGCTGCTT GGAAGAAC  
 1251 CGCAGTCCCG CTACGGGGTG TTCCCTCAAGA CGCAGTCCC GCTGCGAGCT  
 1301 GCGCAGTCCCG CAGCAGCCGG TGTCGTTGCC CGGGAGAACG CCCAGGGCTC  
 1351 TGTGGCGGCC CCGCAGGGAG AGAACACAC ACCCCCCCTC CCTGGTGCAG  
 1401 CTGCTGCCCG AGACACAGAG CCCCTGGCAG GTGTACCGCT TCGTGGGCC  
 1451 CTGCTGCCCG CGCTGGTGC CGCTGGCCCT CTGGGGCTCC AGGCCAAC  
 1501 AACGCCGCTT CCTCAGGAAC ACCAAGAAGT TCATCTCCCT GGGGAAGCAT  
 1551 GCGCAAGCTCT CGTCGAGGA GCTGACCTGG AAGATGAGCG TGCGGAGCT  
 1601 CGCTTGGCTC CGCAGGAGCC CAGGGGTTGG CTGTCGTTCC CGCCGAGAC  
 1651 ACCGCTGCC TGAGGAGAT CTGGCAAGT TCCCTGCACTG GCTGATGAGT  
 1701 GTGTCAGCTG CGAGCTGCTC CGCTCTTCTT TTATATGTC CGGAGAAC  
 1751 GTTTCAAAG AACAGGCTCA TTCTCTACCA GAAGAGTGTG TGAGGCAAGT  
 1801 TGCAAGCAT TGGAAATCAGA CGACCTTGA AGAGGGTGC CGTCGGGAG  
 1851 CTGTCGGAAAG CAGAGGTGAG CGACCATCGG GAAGCCAGGC CGGCCCTGCT  
 1901 GACGTCCAGA CTCCCTCTCA TCCCCAACGG TGAGGGCTG CGGGCATTTG  
 1951 TGAACATGGA CTACGTCCTG GGAGCCAGGA CGTTCGGCAG AGAAAAGAGG  
 2001 GCGGAGCTCT TCACCTCGAG GGTCAGGCA CTGTTCAAGC TGTCAACTA  
 2051 CGAGGGGGCG CGGGGCCCGG GCTCTCTGG CGCTCTGTG CTGGGCTGG  
 2101 ACGATATCCA CAGGGCTCTG CGCACCTTCG TGTCGCTGT CGGGGCCAG  
 2151 GACCGCCCG CGTAGCTTA CTTGTCAAG GTGGATGTA CGGGCGGTA  
 2201 CGACACCATC CCCAGGACA GGTCACCGA GGTCATGCC AGCATCATCA  
 2251 AACCCAGAA CACGTACTGC GTGCGCTGGT ATGCCGTGTT CGAGAAC  
 2301 GCCCATGGC ACGTCGGCAA GGCTCTCAAG AGCCACGCTCT CTACCTTGAC  
 2351 AGACCTCCAG CGGTACATGC GACAGTGTGG GGTCACCTG CAGGAAACA  
 2401 GCCCGCTGAG GGATGCCGTC GTCATCGAGC AGAGCTCCCTC CCTGAATGAG  
 2451 GCCAGCAGTG GCCTCTCGA CGTCTCTTA CGCTTCATGT GCCACCCAGC

FIG. 50

2501 CGTGCGCATC AGGGGAAAGT CCTAACGTCCA GTGCCAGGGG ATCCCGCAGG  
 2551 GCTCCATCT CTCCACGCTG CTCTGCAGCC TGTGCTACGG CGACATGGAG  
 2601 AACAAAGCTGT TTGGGGGAT TCGCGGGAC GGGCTGCTCC TGCCTTGGT  
 2651 GGATGATTTC TTGTTGGTGA CACCTCACCT CACCCACGG AAAACCTTCC  
 2701 TCAGGACCCCT GGTCGGAGGT GTCCCTGAGT ATGGCTCGGT GTGGAACTTG  
 2751 CGGAAGACAG TGGTGAACCTT CCGTGTAGAA GACGAGGCC TGGGTGCA  
 2801 GGCTTTGTTG CAGATGCCGG CCCACGCCCT ATTCCCCCTGG TCGGGCCTGC  
 2851 TGCTGGATAC CCGGACCCCTG GAGGTGCAAGA GCGACTACTC CAAGCTATGCC  
 2901 CGGACCTCCA TCAGAGCCAG TCTCACCTT AACCGCGCTG TCAAGGCTGG  
 2951 GAGGAACATG CGTGCACAAAC TCTTTGGGT CTTGCGGCTG AAGTGTACA  
 3001 GCCCTGTTCTT GGATTTGCAG GTGAACAGCC TCCAGACGGT GTGCAACAC  
 3051 ATCTACAAAGT CCCTCCCTGCT GCAGGGCTAC AGGTTTCACG CATGTTGCT  
 3101 GCAGCTCCCA TTTCATCAGG AAAGTTTGAA GAACCCCCAAC TTTTTCTCTGC  
 3151 GCGTCATCTC TGACACCGCC TCCCTCTGCT ACTCCATCTC GAAGGCAAAG  
 3201 AACCGAGGGG TGTCGGTGGG GGCCAAAGGC GCGGCCGGCC CTCTGCCCTC  
 3251 CGAGGCCCTG CAGTGGCTGTG GCCACCAAGG ATTCTCTGCTC AAAGCTACTC  
 3301 GACACCGTGT CACCTACGTG CCACTCTGG GGTCACTCAG GACAGCCAG  
 3351 ACGCAGCTGA GTCGGAACCTT CCGGGGGACG ACGCTGACTG CCTGGAGGC  
 3401 CGCAGCCAC CCAGGCACTGC CCTCAGACCTT CAAGACCATC CTGGACTGAT  
 3451 GGCCACCCCG CCACAGCCAG GCGGAGAGCA GACACCCAGCA GCCCTGTAC  
 3501 GCCGGGCTCTC AGCTCCCAAG GAGGGAGGGC CGGCCACAC CGAGGCCCGC  
 3551 ACCGCTGGGA GTCTGAGGCC TGAGTGAATC TTGGCCGAG GCTGCGATGT  
 3601 CCGGCTGAAG GCTGAGTGTG CGGGCTGAGGC CTGAGCGAGT GTCCAGCCAA  
 3651 GGGCTGAGTG TCCAGCAAC CTGCGCTCTT CACTTCCCAC CAGGCTGCG  
 3701 CTCGGCTCCA CCCAGGGGCC AGCTTTCTC CACCAAGGAGC CGGGCTTCCA  
 3751 CTCCCCACAT AGGAATAGTC CATCCCCAGA TTGCGCATTG TTCACCCCTC  
 3801 GCCCTGCCCC CCTTGTGCTT CCACCCCCAC CATCCAGGTG GAGACCCCTGA  
 3851 GAAGGACCCCTT GGGAGCTCTC GGAATTGGAG GTGACCAAAG GTGTCAGTT  
 3901 TACACAGGCC AGGACCTCTG ACCTGGATGG GGTCCTCTGT GGGTCAAATT  
 3951 GGGGGAGGGT GCTGTGGGAG TAAATACTG AATATATGAG TTTTCAGTT  
 4001 TTGAAAAAAA AAAAAAAA AAAAAAAA

**FIG. 50**  
(CONTINUED)

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GCAGCGCTGCGTCTGCTGCGCACGTGGGAAGGCCCTGGCCCGGCCACCCCCGGATGCG  
 1 -----+-----+-----+-----+-----+-----+-----+-----+ 60  
 CGTCGCGACGCGAGGACGACGCGCTGCACCCCTGGGACCGGGGGCGGTGGGGCGCTACCG  
  
 a A A L R P A A H V G S P G P G H P R D A -  
 b Q R C V L L R T W E A L A P A T P A M P -  
 c S A A S C C A R G K P W P R P F P P R C R -  
  
 GCGCGCTCCCGCTGCGAGCGCTGGCCTGCTGCTGCGCAGGCCACTACCGCGAGGTGCT  
 61 -----+-----+-----+-----+-----+-----+-----+ 120  
 CGCGCGAGGGGGCGACGGCTCGGACCGCGAGGGACCGACGGTGTGATGGCGCTCACCGA  
  
 a A R S P L P S R A L P A A Q P L P R G A -  
 b R A P R C R A V R S L L R S H Y R E V L -  
 c A L P A A E P C A P C C C A A T T A R C C -  
  
 GCGCGCTGGCCACGTCTGCGGCGCTGGGGGCCAGGGCTGGCGCTGGCGAGCGCG  
 121 -----+-----+-----+-----+-----+-----+-----+ 180  
 CGGGGACGGCTGCAAGCACCGCGCGACCCCGGGTCCCGACCGCGACCGTGTGCGCC  
  
 a A A G H V R A A P G A P G L A A G A A R -  
 b P L A T F V R R L G P Q G W R L V Q R G -  
 c R W P B R S C G A W G P R A G G W C S A G -  
  
 GGACCGGGGGCTTCCGCGCGNTGGTGGCCCANITGCTGCGTGCCTGCGCTGGGANGN  
 181 -----+-----+-----+-----+-----+-----+-----+ 240  
 CCTGGGGCCCGCAAAGGCGCGCNACACCGGGTACAGNACCAACACCGACGGGACCCCTNCN  
  
 a G P G G F P R ? G G P ? ? G V R A L G ? -  
 b D P A A F R A ? V A ? C ? V C V P W ? ? -  
 c T R R L S A R W W P ? A W C A C P G ? ? -  
  
 ANGGCNGCCCCCGCGCCCTCCCTCGCCAGGTGCTCTGCGTAANGANCTGGTGGC  
 241 -----+-----+-----+-----+-----+-----+-----+ 300  
 TNCCGNGGGGGGGGGGGGGGGGGAGGGAAAGGGCGCTCACAGGACGGACTCTINGAACACCG  
  
 a ? A A P R R P L L P P G V L P E ? ? G G -  
 b ? P P A A P S F R Q V S C L ? ? L V A -  
 c G ? P P P P P S A R C P A \* ? ? W W P -  
  
 CGAGGTGCTGCAANANGCTGTGCGANCGGGCGCGAAANAACTGTGCTGGCCTCGGGCTCG  
 301 -----+-----+-----+-----+-----+-----+-----+ 360  
 GGCTCACGAGCTNTGCAACGCTNGCGCCGCGCTNTTGACAGACCGGGAGCCGAAGCG  
  
 a P S A A ? A V R ? R R E ? R A G L R L R -  
 b R V L ? ? L C A ? R G A ? N V L A F G F A -  
 c E C C ? ? C A ? A A R ? T C W P S A S R -  
  
 GCTGCTGGACGGGGCCCAGGGGGCCCCCCCAGGGCTTCAACCCAGCGCTGCGCAGCTA  
 361 -----+-----+-----+-----+-----+-----+-----+ 420  
 CGACGACCTGCCCCGGGGCCCGGGGGGGGCGCTCGGAAGTGTGGTGCAGCGCTCGAT  
  
 a A A G R G P R G P P R G L H H Q R A Q L -  
 b L L D G A R G G P P P E A F T T S V R S Y -  
 c C W T G P A G A P P R P S P P A C A A -  
  
 CCTGCCCCAACACGGTGACCGAACGACTGCGGGGGAGCGGGGGCTGCGTGC  
 421 -----+-----+-----+-----+-----+-----+-----+ 480  
 GGACGGGTGTGCGCACTGGCTGGCTGCGTGAACGCCCCCTGCCCCCGACCCCGACGACGGC  
  
 a P A Q H G D R T A G E R G V G A A A A -  
 b L P N T V T D A L R G S G A W G L L L R -  
 c C P T R \* P T H C G G A G R G G G C C C A -

FIG. 51

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a P R G R R R A G S P A G T L R ? ? C A G -  
 b R V G G D D L V V H L L A R C A ? F V L V -  
 c A W A T T C W F T C W H A A R ? L C W W -  
  
 541 G G N T C C C A G G T G C G C T A C C A N G T G T G O G G G C C G C G C T G T A C C A G C T C G G G C T G C N A C -  
 CC N A G G T C G A C G C G G A T G G T N C A C A C G C C G G C G C G A C A T G G T C G A G G C C C G A C G N T G + 600  
  
 a G S Q L R L P ? V R A A A V P A R R C ? -  
 b ? P S C A Y ? V C G P P L Y Q L G A A T -  
 c ? P A A P T ? C A G R R C T S S A L ? L -  
  
 601 T C A G G C C G G C C C C G G C A C C G C T A N T G G A C C G A A N G C G T C T G G G A T C C A A C G G G C T -  
 A G T C C G G C C G G G G G G T G C G A T N A C C T G G C T T N G C G A C C T A G G T T G C C C G A + 660  
  
 a S G P A P A T R ? W T R ? R L G S N G P -  
 b Q A R P P P H A ? G P E ? V W D D P T G L -  
 c R P G P R H T L ? D P ? A S G I Q R A W -  
  
 661 G G A C C C T A G G G T C A G G G A G G C C G G G T C C C C T G G G C T G C C A G G C C C G G G T C C G A G G A G + 720  
 C C T T G G T A T C G C A G T C C T C G G C C C A G G G G A C C G G A C G G T C G G G C C C A C G G T C C T C C T C  
  
 a G T I A S G R P G S P W A A S P G C E E -  
 b E P \* R Q G G R G P P G L P A P P G A R R R -  
 c N H S V R E Q V G P L G C Q P R V R G G G -  
  
 721 G G C C G G G G C G T G C C A C C G A A T C T C C C G T T G C C C A A G A G G C C C A G G C G T G G C C T G C -  
 C G G G C C C C G G T C A C G G T C G G C T T C A G A C G G C R A C G G T T C T C G G G T C C G C A C C G G C A G + 780  
  
 a A R G Q C C Q P K S A V A Q E A Q A W R C -  
 b R G G S A S R K S P L P K R P R R G A A A -  
 c A G A V P A E V C R C P R G P G V A L P -  
  
 781 C C C T G A G C C G G S A G G G A C C C C G T T G G C A G G G G T T C T G G G C C C A C C C G G C A G G C G C -  
 G G G A C T C G G G C T C G C C T G G G G A A C C C G T C C C C C A G G A C C C G G G T G G G C C G G T C T G G + 840  
  
 a P \* A G A D A R W A G V L G P P G Q D A -  
 b P E P E R T P V P V G Q G S W A H P G R T P -  
 c L S R S G R P L G R G P G P T R A G R L -  
  
 841 T G G A C C G A G T G A C G G T G G T T C T G T G G G T G T C A C C T G C C A G A C C G G C G A A G A A G C C A C + 900  
 A C C T G G C T C A T G G C A C C A A A G A C A C C A C A C G T G G A C G G T C T G G G C C G G T T C T T C G G T G  
  
 a W T E \* P W F L C G V T C Q T R R R S H -  
 b G P S D R G C V V S V P A R P A E E A T -  
 c D R V T V V S V W C H L P D P P K K P P -  
  
 901 C T C T T G G A G G G T G C G T C T C T G G C A C G G G C C A C T C C C A C C C A T C C G T G G G C C C A G C A + 960  
 G A G A A A C C T C C C A C G G A G A G A C C G T G G G T G G G T G G G T A G G C A C C G G G G G T C G T  
  
 a L F G G C A L W H A P L P P I R G P P A -  
 b S L E G A L S G T R H S H P S V G R Q H -  
 c L W R V R S L A R A T P T H P W A A S T -  
  
 961 C C A C G G G G C C C C C A T C C A C A T C C G G G C C A C C A G T C T G G A C A C G C C T T G T C C C C G + 1020  
 G G T G C G C C C G G G G G T A G G T G T A G G C G C G G T G T G C A G G A C C C T G T G C G G A A C A C G G G G C

**FIG. 51**  
(CONTINUED)

*FIG. 51*  
(CONTINUED)

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a S C G P A C A G W C P Q A S G A P G T T -  
 b R A G L P A P A G A P R P L G L Q A Q R -  
 c V R A C L R R L V P P G L W G S R H N E -

1501 AACGCCGCTCCTCAAGAACCCAGAAGTCATCCTCCCTGGGGAAAGCATGCCAAGCTCT  
 TTGCAGCGAAGGAGTCCCTGTGGTCTTCAGTAGAGGGACCCCTTGATCGGTTGAGGA 1560

a N A A S S G T P R S S S P W G S M P S S -  
 b T P L P Q E H Q E V H L P G E A C Q A L -  
 c R R F L R N T K K F I S L G K H A K L S -

1561 CGCTGCAGGACTGACGTGGAGATGAGGCTGCGGGACTGCCCTTGCTGCCAGGAGCC  
 GGCAGCTCCCTGACTGCACCTTACTCGCACGCCCTGAGCGAACCGAGGGCTCGG 1620

a R C R S \* R G R \* A C G T A L G C A G A -  
 b A A G A D V E D E R A G L R L A Q E P -  
 c L Q E L T W K M S V R D C A W L R R S P -

1621 CAGGGGTTGGCTGTGTTCCGGCCCGAGGACCCGCTGCGTGAGGAGATCTGGCCAAGT  
 GTCCCCAACCGACACAGGGCGCTCGGAGCAGCCACTCTAGGACCGGTTCA 1680

a Q G L A V F R P Q S T V C V R R S W P S -  
 b R G W L C S G R R A P S A \* G D P G Q V -  
 c G V G C V P A A E H R L R E E I L A K F -

1681 TCCCTGCACTGGCTGATGAGTGTGTAAGTGCTGAGCTGGCTAGGTCTTCTTATGTCA  
 AGGACGTGACGACTACTCACATCGCAGCTCGAGTCCAGAAAGAAAATACAGT 1740

a S C T G \* V C T S S S C S G L S F M S -  
 b P A L A D E C V R R R A Q V F L L C H -  
 c L H W M S V Y V R V E L L R S F F Y V T -

1741 CGGAGACACGGTTCAAAAGACAGGGCTCTTCTACCGGAGAGTGCTCTGGACCAAGT  
 GCTCTGGCTGAGTCTTCTGAGCTGAGAAAGATGGCTCTCACAGACCTGGTCA 1800

a R R P R F K R T G S F S T G R V S G A S -  
 b G D H V S K E Q A L F L P E E C L E Q V -  
 c E T T F Q K N R R L F F Y R K S V W S K L -

1801 TGCAAAGCATGGAAATCAGACAGCACTTGAGAGGGCTGCAGCTGGGGAACTTGCGGAG  
 ACGTTTGTAACTCTTGTGCTGAGACTCTCCACGTCAGCCCTGACAGACCTTC 1860

a C K A L E S D S T \* R G C S C G S C R K -  
 b A K H W N Q T A E E G A A A G A V G S -  
 c Q S I G I R Q H L K R V Q L R E L S E A -

1861 CAGAGGTCAAGCAGCACTGGGAGCCAGGCCGCCCTGCTGAGCTCCAGACTCGCTTC  
 GTCTCCAGTCCGTCGTAAGCCCTTGCGTCAGGGAGACAGCTGAGGTCTGAGGCGAAGT 1920

a Q R S G S I G K P G P P C \* R P D S A S -  
 b R G Q A A S G S Q A R P A D V Q T P L H -  
 c E V R Q H R E A R P A L L T S R L R F I -

1921 TCCCCAAGGCTGACGGGCTGCGGGATTGTGACATGGACTACGTCGTTGGAGCCAGA  
 AGGGGTTCCGACTGCCGAGCCGGCTAACACTTGATCTGAGCAGCACCCCTCGGTCTT 1980

**FIG. 51**  
(CONTINUED)

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*FIG. 51*  
(CONTINUED)

**FIG. 51**  
(CONTINUED)

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A T T P A M P G P P S E P V S P S T A A -  
 R L L Q L C P D L H O Q S Q S H Q P R L -  
 D Y S S Y A R T S I R A S L T F N R G F -  
 TCAAGGCTGGAGGAACATCGCTGCAGAACCTCTTGGGCTTGCGGCTGAAGTGTACA  
 2941 AGTCGACCCCTCTTGTAGCGAGGTTGAGAACCCAGAACAGCGACTTCACAGTG  
 S R L G G T C V A N S L G S C G \* S V T -  
 Q G W E E H A S Q T L W G L L A A E V S Q -  
 K A G R N M R R K L F G V L R L K C H S -  
 GCCTGTTCTGGATTTGCAAGGTGAAACAGCTCCAGACGGTGTGACCCAACATCTACAGA  
 3001 CGGAAACAGCTAACCTGCTTCAACTGTGGAGGCTGCCAACAGCTGGTTGTAGATGTTCT  
 A C F W I C R \* T A S R R C A P T S T R -  
 P V S S G F Q A G E Q P P D G V W H Q H L Q D -  
 L F L D L Q V N S L Q T V C T N I Y K I -  
 TCCCTCTGCTGCAGCGTACAGGTTTACAGCATGTGCTGACAGCTCCCATTCTACAGC  
 3061 AGGAGAGCACGACTCGCATGTCCAAGATGCTACACAGCAGCTGGGGTAAAGTAGCTG  
 S S C C R R T G F T H V C C S S H F I S -  
 P P A A G V Q V S R M C A A P I S S A -  
 L L Q A Y R F H A C V L Q L P F H Q Q -  
 AAGTTTGGAGAACCCACATTCTGCGCTCATCTGACAGGCTCCCTCTGCT  
 3121 TTCAACACCTTCTGGGTTGTAAGAGGACGGCAGTAGAGACTGTGGCGAGGAGAGA  
 K F G R T P H F S C A S S L T R P P S A -  
 S L E E P H I F P A R H L \* H G L P P L L -  
 V W K N P T F F L R V I S D T A S L C Y -  
 ACTCATCTGAAAGCCAAAGAACCGAGGGATGTCGCTGGGGCCAAAGGGCGCCGCCGCC  
 3181 TGAGGTAGGACTTCTGGTTCTGGCTCATCGACGCCCGGTTCTCCGCGCCGCCGCC  
 T P S \* K P R T Q G C R W G P R A P P A -  
 L H P E S Q E R R D V A G G Q O G R R R P -  
 S I L K A K N A G M S L G A K G H A A G P -  
 CTCTGGCCCTGGAGCGCTCCGACAGTCACCGACACGGCTGGTGTGCTAAGGAGCAGTCTGAG  
 3241 GAGACGGAGGAGCTCCGACAGTCACCGACACGGCTGGTGTGCTAAGGAGCAGTCTGAG  
 L C P P R P C S G C A T K H S C S S \* L -  
 S A L R G R A V A V P P S I P A Q A D S -  
 L P S E A V Q W L C H Q A F P L L K L T R -  
 GACAGCTGGTGTACCTACAGTGGCACTCTGGGTCAGTCAGGACAGCCAGACGGAGCTGA  
 3301 CTGTCGACAGTGGATGACCGTGAAGAACCCAGTAGGTCTGGCTCTGGGTCAGT  
 D T V S P T C H S W G H S G Q P R R S \* -  
 T P C F H L R A T P G P V T Q D S P P D A A E -  
 H R V T Y V P L L G S L R T A Q T Q L S -  
 GTCCGGAGCTCCGGAGCAGCTGACTGCGCTGAGGAGCCAGACCAACCCGGAGCTG  
 3361 GAGGAGCTGGAGGAGCTCCGGAGCAGCTGACTGCGCTGAGGAGCCAGACCAACCCGGAGCTG

**FIG. 51**  
(CONTINUED)

a V G S S R G R R \* L P W R P Q P T R H C -  
 b S E A P G D D A D C P G G R S Q P G T A -  
 c R K L P G T T L T A L E A A A N P A L P -

3421 CCTCAGACTCTAAGACCATCTGGACTGATGGGCCACAGCCAGGGAGAGCA  
 GGAGTCTGAAGTTCTGGTAGGACCTGACTACCGGTGGGGGTGTCGGTCCGGCTCTCGT + 3480

a P Q T S R P S W T D G H P P T A R P R A -  
 b L R L Q D H P G L M A T R P Q P G R E Q -  
 c S D F K T I L D \* W P P A H S Q A E S R -

GACACCCAGCAGCCCTGTCAGCCCGGGCTCTACGTCGGGAGGGAGGGGGCGGCCACAC  
 3481 CTGTGGTCTGGGACAGTGCGGCCAGATGCAGGGTCCCCTCCCGCCGGGTGTG + 3540

a D T S S P V T P G S T S Q G G R G G G P H -  
 b T P A Q L S R P L R P R E G G G A A H T -  
 c H Q Q P C H A G L Y V P G R E G R P T P -

CCAGGGCCGACCCCTGGGACTGACTGAGGCCCTGACTGAGGTGTTGGCCGGGGCTCATGT  
 3541 GGTCCGGGGCTGGGACCCCTGAGACTCOGACTCACTCACAAACCGCTCCGGACGTACA + 3600

a P G P H R W E S E A \* V S V W P R P A C -  
 b Q A R T A G S L R P E \* V F G R G L H V -  
 c R P A P L G V \* G L S E C L A E A C M S -

CGGGCTGAGGCTGAGCTGTCGGCTGAGGCTCTGAGCTGAGCTGTCAGGCCAGGGCTGAGTC  
 3601 GGGCGAGCTTCGAGCTCACAGGCCAACCTCGGACTCTGCTCACAGGGTGGTCCGGACATCAC + 3660

a P A E G \* V S G \* G L S E C P A K G \* V -  
 b R L K A P V S L P H R L A L G S T P G P -  
 c G \* R L S V R L R P E R V S S Q G L S V -

TCCAGCACCTGGCCGCTCTACCTCCCCACAGGCTGGGCTGGCTCAAGGCTCAACCCAGGGCC  
 3661 AGGTCTGTGGACGGCAGAGTGTAGGGGGTGTCCGGACCCGGCCGAGGTGGGGTCCGGG + 3720

a S S T P A V F T S P Q A G A R L H P R A -  
 b P A H L P S S L P H R L A L G S T P G P -  
 c Q H T C R L H F P T G W R S A P P Q G Q -

AGCTTTCTCACCCAGGAGCCGGCTTCCACTCCCCACATAGGAATAGTCATCCCCAGA  
 3721 TCGAAAAGGAGTGGCTCGGGGGAGGTGAGGGGGTGTATCCATTACAGGTAGGGGTCT + 3780

a S F S S P G A R L P L P T \* E \* S I P R -  
 b A F P H Q E P G F H S P H R N S P S P D -  
 c L F L T R S P A S T P H I G I V H P Q I -

TTGGCCATTGTTCAACCCCTGCGGCTTCCTTGCCTTCCACCCCCACATCCAGGTG  
 3781 AAGCGGTAAACAAGTGGGGAGCGGGACGGAGAAAAGGTGGGGTGTAGGTCCAC + 3840

a F A I V H P S P C P P L P S T P T I Q V -  
 b S P L F T P R P A L L C L P P P P S R W -  
 c R H C S P L A L P S F A F H P H H P G G -

GAGACCCCTGAGAAGGACCCCTGGAGCTCTGGAAATTGGAGTGACCAAAGGTGTGCCCTG  
 3841 CTCTGGGACTCTCTGGGACCCCTGAGACCCCTAACCTCACTGGTTCCACACGGGAC + 3900

**FIG. 51**  
(CONTINUED)

a E T L R R T L G A L G I W S D Q R C A L -  
 b R P \* E G P W E L W E F G V T K G V P C -  
 c D P E K D P G S S G N L E \* P K V C P V -

TACACAGGCGAGGAACCTGACACTGGATGAGGTGCGCTTGTTGCAAAATTGGGGGGAGGT  
 3901 ATGTGTCGCGCTCCGGAGCTGGACGTGGACCTAACCCCGAGGACACCCAGTTAACCCCCCTCCA + 3960

a Y T G E D P A P G W G G S L W V K L G G G G -  
 b T Q A R T L H L D G G G P C G S N W G E V -  
 c H R R G P C T W M G V P V G Q I G G R C -

GCTGTGGGAGGTAAAATACITGAAATAATGAGGTTTTTCAAGTTTGAAAAAAGAAAAAAA  
 3961 CGACACCCCTCATTTATGACTTATATACTCAAAAGTCAAAACTTTTTTTTTTTTTT + 4020

a A V G V K Y \* I Y E F F S F E K K K K K -  
 b L W E \* N T E Y M S F S V L K K K K K K K -  
 c C G S K I L N I \* V F Q F \* K K K K K K K -

AAAAAAA  
 4021 ----- 4029  
 TTTTTTTT

a K K K -  
 b K K -  
 c K K -

*FIG. 51*  
 (CONTINUED)

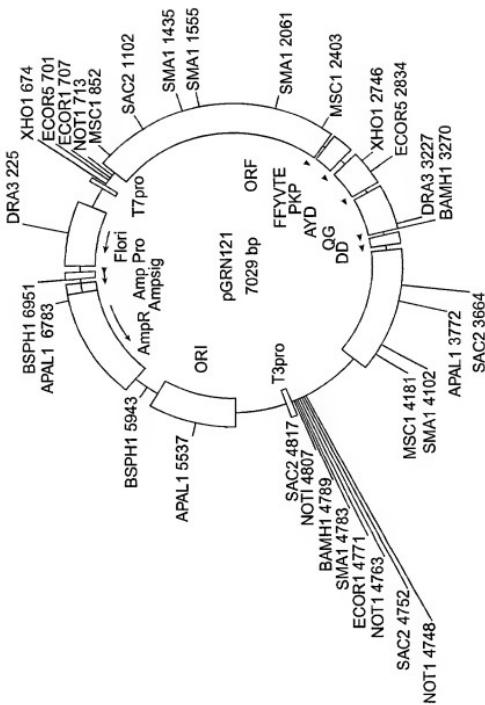


FIG. 52

1  
met  
GCAGCGCTGCGTCTGCTGCGCACGTGGAAGCCCTGGCCCGGCCACCCCCCGCG ATG

10  
pro arg ala pro arg cys arg ala val arg ser leu leu arg ser  
CCG CGC GCT CCC CGC TGC CGA GCC GTG CGC TCC CTG CTG CGC AGC

20  
his tyr arg glu val leu pro leu ala thr phe val arg arg leu  
CAC TAC CGC GAG GTG CTG CCG CTG GCC ACG TTC GTG CGG CGC CTG

30  
gly pro gln gly trp arg leu val gln arg gly asp pro ala ala  
GGG CCC CAG GGC TGG CGG CTG GTG CAG CGC GGG GAC CCG GCG GCT

40  
phe arg ala leu val ala gln cys leu val cys val pro trp asp  
TTC CGC GCG CTG GTG GCC CAG TGC CTC GTG TGC GTG CCC TGG GAC

50  
ala arg pro pro pro ala ala pro ser phe arg gln val ser cys  
GCA CGG CCG CCC CCC GCC GCC CCC TCC TTC CGC CAG GTG TCC TGC

60  
70  
leu lys glu leu val ala arg val leu gln arg leu cys glu arg  
CTG AAG GAG CTG GTG GCC CGA GTG CTG CAG AGG CTG TGC GAG CGC

80  
gly ala lys asn val leu ala phe gly phe ala leu leu asp gly  
GGC GCG AAG AAC GTG CTG GCC TTC GCG TTC GCG CTG CTG GAC GGG

90  
100  
ala arg gly gly pro pro glu ala phe thr thr ser val arg ser  
GCC CGC GGG GGC CCC CCC GAG GCC TTC ACC ACC AGC GTG CGC AGC

110  
120  
tyr leu pro asn thr val thr asp ala leu arg gly ser gly ala  
TAC CTG CCC AAC ACG GTG ACC GAC GCA CTG CGG GGG AGC GGG GCG

130  
140  
trp gly leu leu leu arg arg val gly asp asp val leu val his  
TGG GGG CTG CTG CGC CGC GTG GGC GAC GAC GTG CTG GTT CAC

150  
160  
leu leu ala arg cys ala leu phe val leu val ala pro ser cys  
CTG CTG GCA CGC TGC GCG CTC TTT GTG CTG GTG GCT CCC AGC TGC

170  
180  
ala tyr gln val cys gly pro pro leu tyr gln leu gly ala ala  
GCC TAC CAG GTG TGC GGG CCG CGC CTG TAC CAG CTC GGC GCT GCC

190  
thr gln ala arg pro pro pro his ala ser gly pro arg arg arg  
ACT CAG GCC CGG CCC CCG CCA CAC GCT AGT GGA CCC CGA AGG CGT

FIG. 53

200

leu gly cys glu arg ala trp asn his ser val arg glu ala gly  
CTG GGA TGC GAA CGG GCC TGG AAC CAT AGC GTC AGG GAG GCC GGG

220

val pro leu gly leu pro ala pro gly ala arg arg arg gly gly  
GTC CCC CTG GGC CTG CCA GCC CCG GGT GCG AGG AGG CGC GGG GGC

230

ser ala ser arg ser leu pro leu pro lys arg pro arg arg gly  
AGT GCC AGC CGA AGT CTG CCG TTG CCC AAG AGG CCC AGG CGT CGC

250

ala ala pro glu pro glu arg thr pro val gly gln gly ser trp  
GCT GCC CCT GAG CGG GAG CGG AGC CCC GTT GGG CAG GGG TCC TGG

260

ala his pro gly arg thr arg gly pro ser asp arg gly phe cys  
GCC CAC CCG GGC AGG ACG CGT GGA CCG AGT GAC CGT GGT TTC TGT

270

val val ser pro ala arg pro ala glu glu ala thr ser leu glu  
GTG GTG TCA CCT GCC AGA CCC GCC GAA GAA GCC ACC TCT TTG GAG

290

gly ala leu ser gly thr arg his ser his pro ser val gly arg  
GGT GCG CTC TCT GGC ACG CGC CAC TCC CAC CCA TCC GTG GGC CGC

310

gln his his ala gly pro pro ser thr ser arg pro pro arg pro  
CAG CAC CAC GCG GGC CCC CCA TCC ACA TCG CGG CCA CCA CGT CCC

320

trp asp thr pro cys pro pro val tyr ala glu thr lys his phe  
TGG GAC ACG CCT TGT CCC CGG GTG TAC GCC GAG ACC AAG CAC TTC

340

leu tyr ser ser gly asp lys glu gln leu arg pro ser phe leu  
CTC TAC TCC TCA GGC GAC AAG GAG CAG CTG CGG CCC TCC TTC CTA

350

leu ser ser leu arg pro ser leu thr gly ala arg arg leu val  
CTC AGC TCT CTG AGG CCC AGC CTG ACT GGC GCT CGG AGG CTC GTG

370

glu thr ile phe leu gly ser arg pro trp met pro gly thr pro  
GAG ACC ATC TTT CTG GGT TCC AGG CCC TGG ATG CCA GGG ACT CCC

380

arg arg leu pro arg leu pro gln arg tyr trp gln met arg pro  
CGC AGG TTG CCC CGC CTG CCC CAG CGC TAC TGG CAA ATG CGG CCC

400

leu phe leu glu leu leu gly asn his ala gln cys pro tyr gly  
CTG TTT CTG GAG CTG CTT GGG AAC CAC GCG CAG TGC CCC TAC GGG

410

val leu leu lys thr his cys pro leu arg ala ala val thr pro  
GTG CTC CTC AAG ACG CAC TGC CGG CTG CGA GCT GCG GTC ACC CCA

420

**FIG. 53**  
(CONTINUED)

430  
ala ala gly val cys ala arg glu lys pro gln gly ser val ala  
GCA GCC GGT GTC TGT GCC CGG GAG AAG CCC CAG GGC TCT GTG GCG

440  
ala pro glu glu glu asp thr asp pro arg arg leu val gln leu  
GCC CCC GAG GAG GAC ACA GAC CCC CGT CGC CTG GTG CAG CTG

460  
leu arg gln his ser ser pro trp gln val tyr gly phe val arg  
CTC CGC CAG CAC AGC AGC CCC TGG CAG GTG TAC GGC TTC GTG CGG

470  
ala cys leu arg arg leu val pro pro gly leu trp gly ser arg  
GCC TGC CTG CGC CGG CTG GTG CCC CCA GGC CTC TGG GGC TCC AGG

490  
his asn glu arg arg phe leu arg asn thr lys lys phe ile ser  
CAC AAC GAA CGC CGC TTC CTC AGG AAC ACC AAG AAG TTC ATC TCC

500  
leu gly lys his ala lys leu ser leu gln glu leu thr trp lys  
CTG GGG AAG CAT GCC AAG CTC TCG CTG CAG GAG CTG ACG TGG AAG

520  
met ser val arg asp cys ala trp leu arg arg ser pro gly val  
ATG AGC GTG CGG GAC TGC GCT TGG CTG CGC AGG AGC CCA GGG GTT

530  
gly cys val pro ala ala glu his arg leu arg glu glu ile leu  
GGC TGT GTT CCG GCC GCA GAG CAC CGT CTG CGT GAG GAG ATC CTG

550  
ala lys phe leu his trp leu met ser val tyr val val glu leu  
GCC AAG TTC CTG CAC TGG CTG ATG AGT GTG TAC GTC GTC GAG CTG

560  
leu arg ser phe phe tyr val thr glu thr thr phe gln lys asn  
CTC AGG TCT TTC TTT TAT GTC ACG GAG ACC ACG TTT CAA AAG AAC

580  
arg leu phe phe tyr arg lys ser val trp ser lys leu gln ser  
AGG CTC TTT TTC TAC CGG AAG AGT GTC TGG AGC AAG TTG CAA AGC

590  
ile gly ile arg gln his leu lys arg val gln leu arg glu leu  
ATT GGA ATC AGA CAG CAC TTG AAG AGG GTG CAG CTG CGG GAG CTG

610  
ser glu ala glu val arg gln his arg glu ala arg pro ala leu  
TCG GAA GCA GAG GTC AGG CAG CAT CGG GAA GCC AGG CCC GCC CTG

620  
leu thr ser arg leu arg phe ile pro lys pro asp gly leu arg  
CTG ACG TCC AGA CTC CGC TTC ATC CCC AAG CCT GAC GGG CTG CGG

640  
pro ile val asn met asp tyr val val gly ala arg thr phe arg  
CCG ATT GTG AAC ATG GAC TAC GTC GTG GGA GCC AGA ACG TTC CGC

**FIG. 53**  
(CONTINUED)

650

arg glu lys arg ala glu arg leu thr ser arg val lys ala leu  
AGA GAA AAG AGG GCC GAG CGT CTC ACC TCG AGG GTG AAG GCA CTG

660

phe ser val leu asn tyr glu arg ala arg arg pro gly leu leu  
TTC AGC GTG CTC AAC TAC GAG CGG GCG CGG CCC GGC CTC CTG

670

gly ala ser val leu gly leu asp asp ile his arg ala trp arg  
GGC GCC TCT GTG CTG GGC GAC GAT ATC CAC AGG GCC TGG CGC

680

thr phe val leu arg val arg ala gln asp pro pro pro glu leu  
ACC TTC GTG CTC CGT GTG CGG GCC CAG GAC CCG CCT GAG GAC

690

tyr phe val lys val asp val thr gly ala tyr asp thr ile pro  
TAC TTT GTC AAG GTG GAT GTG ACG GGC GCG TAC GAC ACC ATC CCC

700

gln asp arg leu thr glu val ile ala ser ile ile lys pro gln  
CAG GAC AGG CTC ACG GAG GTC ATC GCC AGC ATC ATC AAA CCC CAG

710

asn thr tyr cys val arg arg tyr ala val val gln lys ala ala  
AAC ACG TAC TGC GTG CGT CGG TAT GCC GTG GTC CAG AAG GCC GCC

720

his gly his val arg lys ala phe lys ser his val ser thr leu  
CAT GGG CAC GTC CGC AAG GCC TTC AAG AGC CAC GTC TCT ACC TTG

730

thr asp leu gln pro tyr met arg gln phe val ala his leu gln  
ACA GAC CTC CAG CGG TAC ATG CGA CAG TTC GTG GCT CAC CTG CAG

740

glu thr ser pro leu arg asp ala val val ile glu gln ser ser  
GAG ACC AGC CCG CTG AGG GAT GCC GTC GTC ATC GAG CAG AGC TCC

750

ser leu asn glu ala ser ser gly leu phe asp val phe leu arg  
TCC CTG AAT GAG GCC AGC AGT GGC CTC TTC GAC GTC TTC CTA CGC

760

phe met cys his his ala val arg ile arg gly lys ser tyr val  
TTC ATG TGC CAC CAC GCC GTG CGC ATC AGG GGC AAG TCC TAC GTC

770

gln cys gln gly ile pro gln gly ser ile leu ser thr leu leu  
CAG TGC CAG GGG ATC CCG CAG GGC TCC ATC CTC TCC ACG CTG CTC

780

cys ser leu cys tyr gly asp met glu asn lys leu phe ala gly  
TGC AGC CTG TGC TAC GGC GAC ATG GAG AAC AAG CTG TTT GCG GGG

790

ile arg arg asp gly leu leu arg leu val asp asp phe leu  
ATT CGG CGG GAC GGG CTG CTC CTG CGT TTG GTG GAT GAT TTC TTG

800

810

820

830

840

850

860

870

**FIG. 53**  
(CONTINUED)

880

leu val thr pro his leu thr his ala lys thr phe leu arg thr  
TTG GTG ACA CCT CAC CTC ACC AAC GCG AAA ACC TTC CTC AGG ACC

890

leu val arg gly val pro glu tyr gly cys val val asn leu arg  
CTG GTC CGA GGT GTC CCT GAG TAT GGC TGC GTG AAC TTG CGG

910

lys thr val val asn phe pro val glu asp glu ala leu gly gly  
AAG ACA GTG GTG AAC TTC CCT GTA GAA GAC GAG GCC CTG GGT GGC

920

thr ala phe val gln met pro ala his gly leu phe pro trp cys  
ACG GCT TTT GGT CAG ATG CCG GCC CAC GGC CTA TTC CCC TGG TGC

940

gly leu leu leu asp thr arg thr leu glu val gln ser asp tyr  
GGC CTG CTG CTG GAT ACC CGG ACC CTG GAG GTG CAG AGC GAC TAC

950

ser ser tyr ala arg thr ser ile arg ala ser leu thr phe asn  
TCC AGC TAT GCC CGG ACC TCC ATC AGA GCC AGT CTC ACC TTC AAC

970

arg gly phe lys ala gly arg asn met arg arg lys leu phe gly  
GGC GGC TTC AAG GCT GGG AGG AAC ATG CGT CGC AAA CTC TTT GGG

980

val leu arg leu lys cys his ser leu phe leu asp leu gln val  
GTC TTG CGG CTG AAG TGT CAC AGC CTG TTT CTG GAT TTG CAG GTG

1000

asn ser leu gln thr val cys thr asn ile tyr lys ile leu leu  
AAC AGC CTC CAG ACC GTG TGC ACC AAC ATC TAC AAG ATC CTC CTG

1010

leu gln ala tyr arg phe his ala cys val leu gln leu pro phe  
CTG CAG GCG TAC AGG TTT CAC GCA TGT GTG CTG CAG CTC CCA TTT

1030

his gln gln val trp lys asn pro thr phe phe leu arg val ile  
CAT CAG CAA GTT TGG AAG AAC CCC ACA TTT TTC CTG CGC GTC ATC

1040

ser asp thr ala ser leu cys tyr ser ile leu lys ala lys asn  
TCT GAC ACG GCC TCC CTC TGC TAC TCC ATC CTG AAA GCC AAG AAC

1060

ala gly met ser leu gly ala lys gly ala ala gly pro leu pro  
GCA GGG ATG TCG CTG GGG GCC AAG GGC GCC GGC CCT CTG CCC

1070

ser glu ala val gln trp leu cys his gln ala phe leu leu lys  
TCC GAG GCC GTG CAG TGG CTG TGC CAC CAA GCA TTC CTG CTC AAG

1080

leu thr arg his arg val thr tyr val pro leu leu gly ser leu  
CTG ACT CGA CAC CGT GTC ACC TAC GTG CCA CTC CTG GGG TCA CTC

**FIG. 53**  
(CONTINUED)

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1100
arg thr ala gln thr gln leu ser arg lys leu pro gly thr thr
AGG ACA GCC CAG ACG CTG AGT CGG AAG CTC CGG GGG ACG ACG AGC

1120
leu thr ala leu glu ala ala asn pro ala leu pro ser asp
CTG ACT GCC CTG GAG GCC GCA AAC CCG GCA CTG CCC TCA GAC

1130      1132
phe lys thr ile leu asp OP
TTC AAG ACC ATC CTG GAC TGA TGGCCACCCGCCACAGCCAGGCCAGAGCAGA
CACCAGCAGCCCTGTCA CGCCGGCTCTACGTCCAGGGAGGGAGGGCGGCCAACACCC
AGGCCCGCACCGCTGGGAGTCTGAGGCCCTGAGTGTAGTGTGTTGCCAGGCCCTGCATGTCC
GGCTGAAGGCTGAGTGTCCGGCTGAGGCTGAGCGAGTGTCCAGCCAAGGGCTGAGTGTCC
CAGCACACCTGCCGTCTTCACTCCCCACAGGTGGCGCTCGCTCCACCCCAGGCCAG
CTTTTCYTCA CACAGGAGCCCGTTCACTCCCCACATAGGAATAGTCATCCCCAGATT
CGCCATTGTTCACCCYTCGCCCTGCCYTCTTGCCTTCACCCCCACATCCAGGTGGA
GACCTGAGAAGGACCTGGAGCTCTGGGAATTGGAGTGACCAAAGGTGTGCCCTGTGA
CACAGGCGAGGACCCCTGCACCTGGATGGGGTCCCTGTGGGTCAAATTGGGGGAGGTGCA
TGTGGGAGTAAATACTGAATATATGAGTTTTCA GTTTTGTGAAAAAAA
AAAAAAAAAA

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*FIG. 53*  
(CONTINUED)

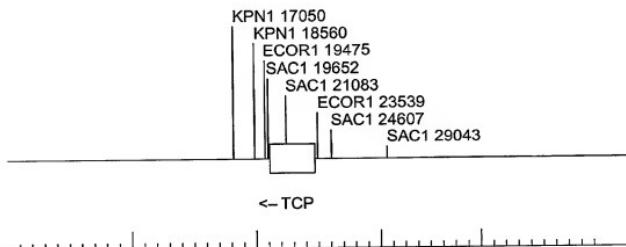


FIG. 54